

From: Bunner, Bridget
Sent: Friday, August 02, 2002 4:31 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

10/10/2000

10/12/1999

09/721,341

8/6 Note: consider making 103
if App. overcomes 112-1

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

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STIC

10321, 10350

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/6
Date Completed: 8/7
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.):
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: as
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:04:30 ; Search time 13.09 seconds
(without alignments)
653.091 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEQNQSTDYVEENEMNG.....VEEFPDSEGTPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1620	99.1	350	2	US-08-966-316-18
3	659	36.2	358	1	US-08-153-848-19
4	659	36.2	358	3	US-09-299-843A-19
5	659	36.2	358	4	US-09-088-337B-19
6	659	36.2	358	5	PCT-US93-11153-19
7	659	36.2	378	1	US-08-153-848-15
8	659	36.2	378	3	US-09-299-843A-15
9	659	36.2	378	4	US-09-251-545-1
10	659	36.2	378	4	US-09-088-337B-15
11	659	36.2	378	5	PCT-US93-11153-15
12	659	36.2	410	1	US-08-153-848-7
13	659	36.2	410	3	US-09-299-843A-7
14	659	36.2	410	4	US-09-088-337B-7
15	659	36.2	410	5	PCT-US93-11153-7
16	650	35.7	378	3	US-09-299-843A-66
17	650	35.7	378	4	US-09-088-337B-66
18	643	35.3	378	1	US-08-383-750-2
19	643	35.3	378	3	US-08-383-751A-2
20	643	35.3	378	3	US-08-352-678-2
21	643	35.3	378	4	US-09-045-583-49
22	643	35.3	378	5	PCT-US93-09636-2
23	637	35.0	357	4	US-09-266-464-2
24	635.5	34.9	359	1	US-08-153-848-24
25	635.5	34.9	359	3	US-09-299-843A-24
26	635.5	34.9	359	4	US-09-088-337B-24
27	635.5	34.9	359	5	PCT-US93-11153-24

28	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appli
29	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appli
30	583	32.1	374	4	US-09-045-583-48	Sequence 48, Appli
31	581	31.9	342	4	US-09-116-498-4	Sequence 4, Appli
32	569	31.3	342	2	US-09-116-498-6	Sequence 6, Appli
33	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appli
34	560	30.8	342	4	US-09-275-384B-5	Sequence 5, Appli
35	560	30.8	342	4	US-09-116-498-2	Sequence 2, Appli
36	560	30.8	342	4	US-09-449-437A-2	Sequence 2, Appli
37	537.5	29.5	360	4	US-08-875-573-20	Sequence 20, Appli
38	537.5	29.5	360	4	US-09-232-878-2	Sequence 2, Appli
39	537.5	29.5	360	4	US-09-045-583-55	Sequence 55, Appli
40	534.5	29.4	355	1	US-07-759-568-1	Sequence 1, Appli
41	534.5	29.4	355	1	US-08-450-393A-8	Sequence 8, Appli
42	534.5	29.4	355	2	US-08-390-000A-5	Sequence 5, Appli
43	534.5	29.4	355	4	US-08-446-669-8	Sequence 8, Appli
44	534.5	29.4	355	5	PCT-US95-00476-8	Sequence 7, Appli
45	534.5	29.4	360	1	US-08-202-056-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-966-316-16
; Sequence 16, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
; US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 7.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60
DB 1 MALEONQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60

QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKITTSALYT 120
DB 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKITTSALYT 120

QY 121 LNFVSGMOFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 LNFVSGMOFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180

QY 181 NARCIPFPRLYLGTSKALIQMLEICIGFVVPFLIMGVCFYFITTARTLMKMPNIIKISRPLK 240
DB 181 NARCIPFPRLYLGTSKALIQMLEICIGFVVPFLIMGVCFYFITTARTLMKMPNIIKISRPLK 240

QY 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300
DB 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300

QY 301 ILYVFMGASFKNYVMKAKYGSRRQRQSVVEEPPFDSEGTPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKAKYGSRRQRQSVVEEPPFDSEGTPTSTFSI 350

RESULT 2
US-08-966-316-18
; Sequence 18, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 7.1e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60
DB 1 MALEONQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60

QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKITTSALYT 120
DB 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKITTSALYT 120

QY 121 LNFVSGMOFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 LNFVSGMOFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180

QY 181 NARCIPFPRLYLGTSKALIQMLEICIGFVVPFLIMGVCFYFITTARTLMKMPNIIKISRPLK 240
DB 181 NARCIPFPRLYLGTSKALIQMLEICIGFVVPFLIMGVCFYFITTARTLMKMPNIIKISRPLK 240

QY 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300
DB 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300

QY 301 ILYVFMGASFKNYVMKAKYGSRRQRQSVVEEPPFDSEGTPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKAKYGSRRQRQSVVEEPPFDSEGTPTSTFSI 350

RESULT 3
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300

```

; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-19

Query Match          36.2%; Score 659; DB 1; Length 358;
Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYVEENMGTYDYSOYELICIKEDYREFAKVFLPVLTVFVIGLAGNS 60
DB 1 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLLNG 57

QY 61 MVVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 58 LVVLTYYIKRLKTDVYLLNLAVALDILFTLPFWAYSAAKSWVGVHFKLIFAIYK 117

QY 121 LNFVSGMQLACISIDRYVAVTKVPS-----QSGVGKPCWICFCVWMAILLISIPQLVY 176
DB 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPELLYS 177

QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVVPFLMGVCVFFITARTLMKMP 231
DB 178 DLORSSSQAMKCSLITEH---VEAFITQVAQWVIGLVPPLANSFCYLVIIRTLQAR 234

QY 232 NIKISRPLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 235 NFERNKAIKIVIAVVFVIFQLPYNGVLAQTVANFNITSSTCELSKQLNIAYDVYSL 294

QY 292 ALFHSCNLPILYVFMGASFKNYVMKAKYK-----SW-----RRQRSVEEFPFD 337
DB 295 ACVRCVNPFLYAFIGVKFRNDLFKLDIGLCSQELQRMSSCRHRRSSMSVE----- 349

QY 338 SEGPTPTSTES 349
DB 350 ---AETTTTFS 357

RESULT 4
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
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; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-19

Query Match          36.2%; Score 659; DB 3; Length 358;
Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYVEENMGTYDYSOYELICIKEDYREFAKVFLPVLTVFVIGLAGNS 60
DB 1 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLLNG 57

QY 61 MVVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 58 LVVLTYYIKRLKTDVYLLNLAVALDILFTLPFWAYSAAKSWVGVHFKLIFAIYK 117

QY 121 LNFVSGMQLACISIDRYVAVTKVPS-----QSGVGKPCWICFCVWMAILLISIPQLVY 176
DB 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPELLYS 177

QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVVPFLMGVCVFFITARTLMKMP 231
DB 178 DLORSSSQAMKCSLITEH---VEAFITQVAQWVIGLVPPLANSFCYLVIIRTLQAR 234

QY 232 NIKISRPLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 235 NFERNKAIKIVIAVVFVIFQLPYNGVLAQTVANFNITSSTCELSKQLNIAYDVYSL 294

QY 292 ALFHSCNLPILYVFMGASFKNYVMKAKYK-----SW-----RRQRSVEEFPFD 337
DB 295 ACVRCVNPFLYAFIGVKFRNDLFKLDIGLCSQELQRMSSCRHRRSSMSVE----- 349

QY 338 SEGPTPTSTES 349
DB 350 ---AETTTTFS 357

RESULT 5
US-09-088-337B-19
; Sequence 19, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
```

```

;
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19

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Query Match 36.2%; Score 659; DB 4; Length 358;

Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNSQDYEEENMGTYDYQYELICIKEDVREFAKVLPLVLTIVFVIGLAGNS 60
Db 1 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKDVRFKAWFLPTMYSIICFVGLLNG 57
QY 61 MVVAIYAYKKQRTDVTYILNLAVADLLFTLPFWAVNAVHGVWLGKIMCKITSALT 120
Db 58 LVVLYIYFKRLKTDYTLNLAVADILFTLPFWAYSAKSWVGVHFKLIFAIYK 117
QY 121 LNFVSGMFLACISIDRYVAVTKVPS---QSGVGKPCWIIICFCVWMAAILLSIPQLV 176
Db 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIP 177
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGVFWPFLMGVCYFITARTLM 231
Db 178 DLQSSSQAMRCSLITEH---VEAFITQVAQWVIGLVLPLAMSCFCLYVIRTLQAR 234
QY 232 NIKSRPLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIOVTSI 291
Db 235 NFERKAIKVIIVVIVFIVTQLPYNGVLAQTVANFNITSTCSELSQLNIAVDVTS 294
QY 292 ALFHSLNPILYVFMGAFKYNVMKAKYK-----SW-----RRQRSVEEFPD 337
Db 295 ACVRCVNPFLYAFYGVKFRNDLFKFLDGLCLSOEQLROWSSCHIRRSSMVE----- 349
QY 338 SEGTEPTSTFS 349
Db 350 ---AETTTFS 357

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RESULT 6

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PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.

```

```

; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Garstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-19

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Query Match 36.2%; Score 659; DB 5; Length 358;

Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNSQDYEEENMGTYDYQYELICIKEDVREFAKVLPLVLTIVFVIGLAGNS 60
Db 1 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKDVRFKAWFLPTMYSIICFVGLLNG 57
QY 61 MVVAIYAYKKQRTDVTYILNLAVADLLFTLPFWAVNAVHGVWLGKIMCKITSALT 120
Db 58 LVVLYIYFKRLKTDYTLNLAVADILFTLPFWAYSAKSWVGVHFKLIFAIYK 117
QY 121 LNFVSGMFLACISIDRYVAVTKVPS---QSGVGKPCWIIICFCVWMAAILLSIPQLV 176
Db 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIP 177
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGVFWPFLMGVCYFITARTLM 231
Db 178 DLQSSSQAMRCSLITEH---VEAFITQVAQWVIGLVLPLAMSCFCLYVIRTLQAR 234
QY 232 NIKSRPLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIOVTSI 291
Db 235 NFERKAIKVIIVVIVFIVTQLPYNGVLAQTVANFNITSTCSELSQLNIAVDVTS 294
QY 292 ALFHSLNPILYVFMGAFKYNVMKAKYK-----SW-----RRQRSVEEFPD 337
Db 295 ACVRCVNPFLYAFYGVKFRNDLFKFLDGLCLSOEQLROWSSCHIRRSSMVE----- 349
QY 338 SEGTEPTSTFS 349
Db 350 ---AETTTFS 357

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RESULT 7
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE: 17-NOV-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 7.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSQTDYVEENMGTYDYSOYELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60
DB 21 VCLCODEVDDYIGDNT---TVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLLNG 77

QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVGLKIMCKITSALYT 120
DB 78 LVVLIYIFKRLKTDVTLNLAVADILFLTLFPWAYSAKSWFGVHFCKLIFAIYK 137

QY 121 LNFVSGMQFLACISIDRYVAVTKVPS-----QSGVGKPCWIIICFCVWMAAILLSIPOLVY 176
DB 138 MSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVRLIISKLSGVGIWILATVLSIPELLYS 197
QY 177 TVNDNA----RCIPFPRLYTSNKALIQMLEICIGFVVPFLIMGVCFITARTLMKMP 231
DB 198 DQSRSEQAMKCSLITEH---VEAFITIQVAQMIGFLVPLPMSFCFVLIIRTLQAR 254

QY 232 NIKISRLPKVLLTVIVFVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSI 291
DB 255 NFERNAKIVIAVVFVIFQLPYNGVLAQTVANFNITSTCELSKOLNAYDVYISL 314

QY 292 ALPHSCLNPILYVFMGASKNYVMKVKYG-----SW-----RRQRSVEEFPD 337
DB 292 ALPHSCLNPILYVFMGASKNYVMKVKYG-----SW-----RRQRSVEEFPD 337

DB 315 ACVRCCVNPFLYAFICGVKFRNDLFKLFKDLGCLSQBLQWSSCRHRRSSMSVE----- 369
QY 338 SEGPTPTSTFS 349
DB 370 ----AETTTTFS 377

RESULT 8
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 7.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSQTDYVEENMGTYDYSOYELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60
DB 21 VCLCODEVDDYIGDNT---TVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLLNG 77

QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVGLKIMCKITSALYT 120
DB 78 LVVLIYIFKRLKTDVTLNLAVADILFLTLFPWAYSAKSWFGVHFCKLIFAIYK 137

QY 121 LNFVSGMQFLACISIDRYVAVTKVPS-----QSGVGKPCWIIICFCVWMAAILLSIPOLVY 176


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QY 61 MVAIAIYAYKKQRTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSALYT 120
Db 110 LVLTIIYIFKRLKMTDITLLNLAVADILFLTLFPWAYSAKSWVFGVHFKLIFAIYK 169
QY 121 LNFVSGMQFIACISIDRYVAVTKVPs-----QSGVGKPCWIIICFCVWMAAILLSIPOLVFY 176
Db 170 MSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLSVGVILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPYLGTSKALQMLEICIGFVVPFLINGCYFITARTLMKMP 231
Db 230 DLQSSSEQAMRCSLITEH---VEAFITIOVQOMVIGFLVPLLAMSFCYLVITRTLLQAR 286
QY 232 NIKISRLKVLTVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKSRMDIAIQVTESTI 291
Db 287 NFERNAIKAVIIAVVVFVQLPYNGVVLQAVANFNITSTCSELSKQLNIADVTYSL 346
QY 292 ALPHSCNLPILVFVGASPKNYVMKVKYK-----SW-----RRQRSVEEFPFD 337
Db 347 ACVRCVNFPLFAFGVKFRNDFLKFGLDGLCSOEQLRQWSSCRHRRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
Db 402 ----AETTTTFS 409

RESULT 13
US-09-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELE:
; INFORMATION FOR SEQ ID NO: 7:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-7
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Query Match 36.2% Score 659; DB 3; Length 410;
Best Local Similarity 38.7% Pred. No. 7.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALQONOSTDYIYENENMGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Db 53 VCCQDEVTDYIGDNT---TVDYTLFESLCSKKDVRNFKANFLPIMYSIICFVGLLNG 109
QY 61 MVAIAIYAYKKQRTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSALYT 120
Db 110 LVLTIIYIFKRLKMTDITLLNLAVADILFLTLFPWAYSAKSWVFGVHFKLIFAIYK 169
QY 121 LNFVSGMQFIACISIDRYVAVTKVPs-----QSGVGKPCWIIICFCVWMAAILLSIPOLVFY 176
Db 170 MSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLSVGVILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPYLGTSKALQMLEICIGFVVPFLINGCYFITARTLMKMP 231
Db 230 DLQSSSEQAMRCSLITEH---VEAFITIOVQOMVIGFLVPLLAMSFCYLVITRTLLQAR 286
QY 232 NIKISRLKVLTVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKSRMDIAIQVTESTI 291
Db 287 NFERNAIKAVIIAVVVFVQLPYNGVVLQAVANFNITSTCSELSKQLNIADVTYSL 346
QY 292 ALPHSCNLPILVFVGASPKNYVMKVKYK-----SW-----RRQRSVEEFPFD 337
Db 347 ACVRCVNFPLFAFGVKFRNDFLKFGLDGLCSOEQLRQWSSCRHRRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
Db 402 ----AETTTTFS 409
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RESULT 14
US-09-088-337B-7
; Sequence 7, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-JUN-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-337B-7

Query Match 36.2%; Score 659; DB 4; Length 410;
Best Local Similarity 38.7%; Pred. No. 7.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEQNSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVFLPVELTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---TVDYTLFESLCKSKDVRNFKAWFLPIMYSIIICFVGLLNG 109
QY 61 MVVAIYAYKKQRTDYYILNLAVALDLLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 110 LVWLYIYFKRLKWTDTYLLNLAVALDILFLLTLPFWAYSAAKSWVGVHFCCLIFAIYK 169
QY 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGKPCWICFCVWMAAILLSIPOLVY 176
DB 170 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLCVGIWILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVWPFLMGVCYFETARTLMKMP 231
DB 230 DLQSSSQAMRCSLITEH---VEAFITQVQMVIGFLVPLAMSFCYLVIIIRTLQAR 286
QY 232 NIKISRLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 287 NFERNKAIVIAVVVVFVQLPYNGVVLQAVANFNITSSCTELSKQLNIAYDVTYSL 346
QY 292 ALFHSCNLPILYVFMGASFKNYVMKVAKYG-----SW-----RRQRQSVVEEPPFD 337
DB 347 ACVRCVNPFLYAFYGVKFRNDLFLKFDGLCLSQBLQWSSCRHRRSSMSVE-----401
QY 338 SEGPTPTSTFS 349
DB 402 ----AETTTTFS 409

RESULT 15
PCT-US93-11153-7
Sequence 7, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-7
Query Match 36.2%; Score 659; DB 5; Length 410;
Best Local Similarity 38.7%; Pred. No. 7.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEQNSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVFLPVELTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---TVDYTLFESLCKSKDVRNFKAWFLPIMYSIIICFVGLLNG 109
QY 61 MVVAIYAYKKQRTDYYILNLAVALDLLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 110 LVWLYIYFKRLKWTDTYLLNLAVALDILFLLTLPFWAYSAAKSWVGVHFCCLIFAIYK 169
QY 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGKPCWICFCVWMAAILLSIPOLVY 176
DB 170 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLCVGIWILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVWPFLMGVCYFETARTLMKMP 231
DB 230 DLQSSSQAMRCSLITEH---VEAFITQVQMVIGFLVPLAMSFCYLVIIIRTLQAR 286
QY 232 NIKISRLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 287 NFERNKAIVIAVVVVFVQLPYNGVVLQAVANFNITSSCTELSKQLNIAYDVTYSL 346
QY 292 ALFHSCNLPILYVFMGASFKNYVMKVAKYG-----SW-----RRQRQSVVEEPPFD 337
DB 347 ACVRCVNPFLYAFYGVKFRNDLFLKFDGLCLSQBLQWSSCRHRRSSMSVE-----401
QY 338 SEGPTPTSTFS 349
DB 402 ----AETTTTFS 409
Search completed: August 6, 2002, 18:08:28
Job time: 238 sec

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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:07:30 ; Search time 13.42 Seconds
(without alignments)
1009.824 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNSTDYEEENMG.....VEEPFDSEGTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1819	100.0	350	1	CKRB_HUMAN	Q9nbp9 homo sapien
2	1620	89.1	350	1	CKRB_BOVIN	P35350 bos taurus
3	659	36.2	378	1	CKR7_HUMAN	P32248 homo sapien
4	650	35.7	378	1	CKR7_MOUSE	P47774 mus musculus
5	639	35.1	369	1	CKR9_MOUSE	Q9wtu7 mus musculus
6	637	35.0	357	1	CKR9_HUMAN	P51686 homo sapien
7	605	33.3	367	1	CKR6_MOUSE	O54689 mus musculus
8	583	32.1	374	1	CKR6_HUMAN	P51684 homo sapien
9	581	31.9	342	1	CCRE_CERAE	O18983 cercopithec
10	571	31.4	343	1	CKR6_MACMU	Q9xt45 macaca mula
11	569	31.3	342	1	CCRE_MACNE	O19024 macaca neme
12	560	30.8	342	1	CKR6_HUMAN	O00574 homo sapien
13	537.5	29.5	360	1	CKR4_HUMAN	P51679 homo sapien
14	534.5	29.4	360	1	IL8B_HUMAN	P25025 homo sapien
15	529.5	29.1	353	1	IL8B_PANTR	Q28807 pan troglod
16	525	28.9	362	1	CKRA_HUMAN	P46092 homo sapien
17	524	28.8	354	1	C3X1_RAT	P35411 rattus norv
18	523	28.8	384	1	CKD6_HUMAN	O00590 homo sapien
19	522.5	28.7	353	1	IL8B_GORGO	Q28422 gorilla gor
20	522.5	28.7	355	1	C3X1_HUMAN	P49238 homo sapien
21	522.5	28.7	360	1	CKR4_MOUSE	P51680 mus musculus
22	521.5	28.7	353	1	IL8B_MACMU	Q28519 macaca mula
23	520.5	28.6	362	1	CKRA_MOUSE	Q9j121 mus musculus
24	512	28.1	356	1	IL8B_CANFA	Q97571 canis famil
25	511	28.1	354	1	C3X1_MOUSE	Q9z0d9 mus musculus
26	511	28.1	358	1	IL8B_RABIT	P35344 cryotolagus
27	504	27.7	360	1	CKR2_MACMU	O18793 macaca mula
28	501.5	27.6	355	1	IL8A_RABIT	P21109 oryctolagus
29	501.5	27.6	358	1	CKR3_CAVPO	Q9z213 cavia porce
30	500.5	27.5	352	1	CKR4_HUMAN	P30991 homo sapien
31	499.5	27.5	353	1	CKR4_BOVIN	P25930 bos taurus
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33	498.5	27.4	352	1	CKR4_PAPAN	P56491 papio anubi

RESULT	1	CKRB_HUMAN	STANDARD;	PRT;	350 AA.
ID	Q9NPB9;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	C-C chemokine receptor type II (C-C CKR-11) (CC-CKR-11) (CCR-11)				
DE	(Chemokine receptor-like 1) (CCL1) (CCX CKR).				
GN	CCR11 OR CCRP2 OR VSHK1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20200450; PubMed=10734104;				
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;				
RT	"CCR11 is a functional receptor for the monocyte chemoattractant				
RT	protein family of chemokines.";				
RL	J. Biol. Chem. 275:9550-9556(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20171478; PubMed=10706668;				
RA	Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,				
RT	Schall T.J.;				
RT	"Cutting edge: identification of a novel chemokine receptor that binds				
RT	dendritic cell- and T cell-active chemokines including ELC, SLC, and				
RT	TECK.";				
RL	J. Immunol. 164:2851-2856(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20231748; PubMed=10767544;				
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;				
RT	"Cloning of CCR11, an orphan seven transmembrane receptor related to				
RT	chemokine receptors, expressed abundantly in heart.";				
RL	Gene 246:223-238(2000).				
CC	-1- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.				
CC	SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER				
CC	EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL				
CC	TISSUES.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF193507; AAF61299.1; -				
DR	EMBL; AF233281; AAF44751.1; -				
DR	EMBL; AF110640; AAF59827.1; -				

062743 cercocobus
P56498 felis silve
P55919 gorilla gor
P56493 cercopithec
062747 cercocobus
Q28474 macaca fasc
P79394 macaca mula
O54814 rattus norv
P35407 rattus norv
P56441 papio hamad
O97880 pygathrix b
P79436 macaca mula

ALIGNMENTS

```

DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 107 POTENTIAL.
FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 134 POTENTIAL.
FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 POTENTIAL.
FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 290 310 POTENTIAL.
FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D25757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVPFLVFTIVFVIGLAGNS 60
DB 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVPFLVFTIVFVIGLAGNS 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPKSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 LNFVSGMQFLACISIDRYAVATKVPKSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
QY 181 NARCIPIFRYLGTSMKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240
DB 181 NARCIPIFRYLGTSMKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240
QY 241 VLLTIVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNKRMDIAIOVTESIALFHSCLNP 300
DB 241 VLLTIVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNKRMDIAIOVTESIALFHSCLNP 300
QY 301 ILVYFGASFKNYVMKAKYIGSWRRQRQSVVEFPDSEGTPTSTFSI 350
DB 301 ILVYFGASFKNYVMKAKYIGSWRRQRQSVVEFPDSEGTPTSTFSI 350

RESULT 2
CKRB_BOVIN STANDARD; PRT; 350 AA.
AC P35350;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-CR-11) (CC-CR-11) (CCR-11)
DE (Possible gustatory receptor type B) (PPRI protein).
GN CCR11.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

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RC Tissue=Tongue;
RX MEDLINE-93326166; PubMed-8392843;
RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;
RT "Identification of novel members of G-protein coupled receptor
RL superfamily expressed in bovine taste tissue.";
RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.
CC -!- SUBCELLULAR LOCATION: Integrated membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S63848; AAB27547.1; -.
DR PIR; JN0621; JN0621.
DR GCRdb; GCR_0757; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW phosphorylation.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 66 1 (POTENTIAL).
FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 135 3 (POTENTIAL).
FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 306 7 (POTENTIAL).
FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.8e-92;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVPFLVFTIVFVIGLAGNS 60
DB 1 MAVEYQSDYDYIYENENMGTYDSQVELICIKEDVREFAKVPFLVFTIVFVIGLAGNS 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 TVVAIYAYKKRRTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPKSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 LNFVSGMQFLACISIDRYAVATKVPKSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
QY 181 NARCIPIFRYLGTSMKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240
DB 181 KARCVPFIFHYLGTSMKASIQILEICIGFIFPLIMAVCYFITAKTLIMPNKISRPLK 240

```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RP STRAIN=B6/CBA; TISSUE=Thymus;
 RC MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Report C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse Ebt1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L31580; AAA74232.1; -;
 DR MGD; MGI:103011; Cnkb7.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
 FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 60 86 1 (POTENTIAL).
 FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 116 2 (POTENTIAL).
 FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 131 152 3 (POTENTIAL).
 FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 4 (POTENTIAL).
 FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 220 247 5 (POTENTIAL).
 FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 264 289 6 (POTENTIAL).
 FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 314 331 7 (POTENTIAL).
 FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 129 210 BY SIMILARITY.
 SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AA54 CRC64;

Query Match 35.7%; Score 650; DB 1; Length 378;
 Best Local Similarity 38.3%; Pred. No. 2.6e-33;
 Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNOSTDYEEENMGTYDSQYELICKEVDREFAKVLFPVELTIVFVIGLAGNSMVA 64
 DB 25 ODEVTDDYIGENT---TVDYTLVESVCFKDVNRKAWFLPLMVSIVCFVGLLGNGLVIL 81
 QY 65 IYAYKKORTKTDVYILANLAVALLLLTLPFVAVNAVHGVGLKIMKITSALYTLNFV 124
 DB 82 TYIYFKRLKMTDYLNLAVADLLFLLPFWAYSEAKSWIFGVLCKGFGFYKLSFF 141
 QY 125 SGWFLACISIDRYAVTKVPSQS-----VGKPCWILGFCVYMAILLSPILVYFT 177
 DB 142 SGMLLLLCISIDRYVAIVQVSRHRHARVLLISK---LSCVGIWMLALFELSPILYS 198
 QY 178 VDNA-----RCIFPFLYGLTSKAL--IQMLEICIGFVVPFLMGVGYFIFARTLMKM 230
 DB 199 LQKNSGDTLRC-----SLVSAQVEALITIQVAQMFGLVPLMAMSFVCLIIIRTLQA 253

QY 231 PNIKISRLKVLTLVWIVETQLPYNIVKFCRAIDIIYSLITSCNMSKRMDAIOVTES 290
 DB 254 RNFRNKAIKVIIVAVVVFVIFQLPYNGVVAQTVANFNITNSCETS KOLNAYDVYTS 313
 QY 291 IALFHSCLNPLXYFMGASPKNYVMKVKYKGSRROR-----OSVEEFPPDSECPTE 343
 DB 314 LASVRCVNPFLYAFVIGKFRSDFLKLFDGLCLSQERLHRHWSCHRVNASVSME--AE 371
 QY 344 PTSTFS 349
 DB 372 TTTTFS 377

RESULT 5
 CKR9_MOUSE
 ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WUT7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
 DE (Chemokine C-C receptor 10).
 GN CCR9 OR CCKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballo A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: Identification of the orphan chemokine receptor GPR-9-6
 RL as CCR9, the receptor for the chemokine TECK";
 RL J. Immunol. 162:5671-5675(1999).
 CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AJ132336; CAB43480.1; -;
 DR MGD; MGI:1341902; Cnkb10.
 DR InterPro; IPR004069; Chemokine9_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR01531; CHEMOKINER9.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 76 1 (POTENTIAL).
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 2 (POTENTIAL).
 FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181 4 (POTENTIAL).
 FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 238 5 (POTENTIAL).
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).

[illegible]

CC -|- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -|- INDUCTION: BY INTERLEUKIN-2.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -|- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
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CC -----
DR EMBL; U45984; AAB62714.1; -;
DR EMBL; 249784; CAB02144.1; ALT_INIT.
DR EMBL; U60000; AAB06949.1; -;
DR EMBL; U68030; AAC51124.1; -;
DR EMBL; U68032; AAC51125.1; -;
DR HSSP; P34996; 1DD0.
DR GCRDb; GCR_1037; -;
DR GCRDb; GCR_1075; -;
DR GCRDb; GCR_1906; -;
DR GCRDb; GCR_1919; -;
DR GCRDb; GCR_1941; -;
DR GCRDb; GCR_2110; -;
DR MIM; 601835; -;
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR004067; Chemokine6_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01529; CHEMOKINER6.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 83
FT TRANSMEM 84 104
FT TRANSMEM 105 119
FT TRANSMEM 120 141
FT TRANSMEM 142 159
FT TRANSMEM 160 180
FT TRANSMEM 181 211
FT TRANSMEM 212 238
FT TRANSMEM 239 254
FT TRANSMEM 255 279
FT TRANSMEM 280 303
FT TRANSMEM 304 321
FT TRANSMEM 322 374
FT DISULFID 118 197
FT CARBOHYD 7 7
FT CARBOHYD 23 23
FT CONFLICT 60 60
FT CONFLICT 74 74
FT CONFLICT 86 86
FT CONFLICT 164 164
FT CONFLICT 182 182
FT CONFLICT 192 192
FT CONFLICT 206 206
FT CONFLICT 225 225
FT CONFLICT 370 374
FT CONFLICT 374 374
SQ SEQUENCE 374 AA; 42494 MW; DTF963534E990BC4 CRC64;
Query Match 32.1%; Score 583; DB 1; Length 374;
Best Local Similarity 36.1%; Pred. No. 3.2e-29;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;
OY 8 STDYEEENEMNGTYDYSOYELICIKEDVREPAKFLPVFLTFIVFVIGLAGNSMVVAIYA 67

Db 23 NTSYSDSEM-----LLCSLQEQRSRLFPVPIAYSILICVGLGNILVITEA 72
QY 68 YKKKORTKTDVYILNAVADLLLTLPFWAV-NAVHGVLGKIMCKITSALYTLNFVS 126
Db 73 FYKKARSMTDYYLLNMAIADILFVLTLPFWAVSHGAWFVSNAATCKLKGIAINFNGC 132
QY 127 MOFLACISIDRYVAVTKVPS-----OSGVGKPCWIIICFCVMAAILLSIPQLVF---YTVN 179
Db 133 MLLLTACISMDRYIAIVQATKSPRLRSRTLPKSKICLVVWGLSVIISSTFEVFNQYNTQ 192
QY 180 DNARCIPIPRYLGRS-----MKALQMLBICIGFVVPLFMGVCFITARTLMKMPNIIK 235
Db 193 GSDVC---EPKYQTVSEPIRWKLLMLGLELLEFFPLFMFMICYFTFIVKTLVQAQNSR 249
QY 236 SRPLKVLTLVTVIVTQLPYNIVKFCRAIDIIYISLITSCNMSKRMIDIAIQVTESTALFH 295
Db 250 HKAIRVITIAVLVFLACQIPHNNVLLVTAAN-LGKNRSCQSEKLGIGYTKVTVEVLAFLH 308
QY 296 SCLNPILYVFMGASPKNYVMVAKKYGSWRQRQS 330
Db 309 CCLNPVLYAFIGQKERNYFLKILKDLWCVRKYKS 343
RESULT 9
ID CCR6_CERAE STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo).
GN CXCR6 OR BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewairamani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -|- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF007859; AAB64225.1; -;
DR GCRDb; GCR_2411; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT TRANSMEM 60 68
FT TRANSMEM 69 89
FT TRANSMEM 90 103
FT TRANSMEM 104 125
FT TRANSMEM 126 125


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DR EMBL; AB023890; BAA86967.1; -.
DR EMBL; AB023891; BAA86968.1; -.
DR EMBL; AB023892; BAA86969.1; -.
DR GCRDb; GCR_2115; -.
DR MIM; 604836; -.
DR InterPro; IPR000276; GPCR_Rhodospn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Polymorphism.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 67 1 (POTENTIAL).
FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 98 2 (POTENTIAL).
FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 176 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 267 6 (POTENTIAL).
FT DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 285 308 7 (POTENTIAL).
FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT VARIANT 130 130 L -> V.
FT VARIANT 178 178 /FTIG-VAR_010669.
FT VARIANT 178 178 C -> S.
FT VARIANT 178 178 /FTIG-VAR_010670.
SQ SEQUENCE 360 AA; 41402 MW; 51EBE12AD1FAFABP CRC64;

Query Match 29.5%; Score 537.5; DB 1; Length 360;
Best Local Similarity 35.8%; Pred. No. 1.8e-26;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

QY 10 DYVYENENMGNYDYSQYELICIKEDVREFAKVFVFTVVFVIGLAGNSWVAIYAY 69
DB 8 DTTLESIYSNLYSIESIPKPKTEKIGAFGLPPLYSLVFVGLGNSVVVLVLFY 67

QY 70 KKORTDVIYILNVLADLLLTLPFAVNAVHGVGLKICKITFSAIYTLNLFVSGMOF 129
DB 68 KRLRSTWYLLNLAISDLLFVFSLPFGWGYAQQWVFGLGCKMISWYLVGYSGIFF 127

QY 130 LACISIDRYVAVTKV-----PSQSGVGKPCWIIICFCVYMAAILLSIPQLVF---YTVN 179
DB 128 VMLMSIDRYLAIVHAFVSURARTLTGV-----ITSLATWSAVAFASLPGLFSTCYTER 182

QY 180 DNARCIPFPRVLGTSKKAQLQMLEI-CIGFVVPFLMGVCYFVITARTLMKPNKISRP 238
DB 183 NHTYCTKYS--LNSWTWVLSLENIILGVIPLGIMLCFYSMIIRTLQHCNKNEKKA 240

QY 239 LKVLTVWIVFVITQLPYNVFRCAIDIIYSLITSNCKSRMDIAIQVTESTALFHSCL 298
DB 241 VKMIFAVVVLFGFTWPTYNIVLFLETL-VELEVLQCTERYLDYAIQATETLAFVHCCL 299

QY 299 NPLIYVFMGASPKNYVMKYAK 319
DB 300 NPIIYFELGKPKRYILQLFK 320

RESULT 14
IL8B_HUMAN
ID IL8B_HUMAN STANDARD; PRT; 360 AA.
AC P25025;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA receptor) (IL-8 receptor type 2) (CDw128b).

IL8RB OR CXCR2.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

Murphy P.M., Tiffany H.L.; PubMed=1891716;

"Cloning of complementary DNA encoding a functional human interleukin-8 receptor.";

Science 253:1280-1283(1991).

[2]

SEQUENCE FROM N.A., AND CHARACTERIZATION.

MEDLINE=93205012; PubMed=8384312;

Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P., Beckmann M.P.;

"Molecular characterization of receptors for human interleukin-8, GRO/melanoma growth-stimulatory activity and neutrophil activating peptide-2.";

Mol. Immunol. 30:359-367(1993).

[3]

SEQUENCE FROM N.A.

MEDLINE=94209273; PubMed=7512557;

Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;

"Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.";

J. Biol. Chem. 269:11065-11072(1994).

[4]

SEQUENCE FROM N.A.

TISSUE=Placenta;

MEDLINE=95014476; PubMed=7929358;

Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;

"Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.";

J. Biol. Chem. 269:26381-26389(1994).

[5]

CHARACTERIZATION.

MEDLINE=92355587; PubMed=1379593;

Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;

"Characterization of two high affinity human interleukin-8 receptors.";

J. Biol. Chem. 267:16283-16287(1992).

-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

-!- DATABASE: NAME=PROW; NOTE=CD guide CDw128b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".

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EMBL; M73969; AAA83148.1; -

EMBL; M94582; AAA36108.1; -

EMBL; M99412; AAC14460.1; -

EMBL; L19593; AAB59437.1; -

EMBL; U11869; AAB60656.1; -

PIR; A39446; A39446.

PIR; A53611; A53611.

HSSP; P34996; IDDD.

GCRDb; GCR_0077; -.

Qy	118	LYTLNFVSGHQFLACISIDRYAV---TKVPSSGVCKPCWICICFVWMAAILLSIPQLV	174
Db	122	LKEVYSGILLACLSVDRLAIVHATFTLTKQRY--LVKFTICLSIGLSLLALLPVLL	179
Qy	175	F---YTVNDNARCIPFPRYLG---TSMKALITOMLEICIGFVWPLLMGVCFYFATRL	227
Db	180	FRTVYSSNVSPACY----EDMGNNNTANWRMLLRMLPQSGFGFIVPLLLIMFCYGFTRL	235
Qy	228	MKMPNIKISRPLKVLTLVTVFIVTQLPYNIYVKFCRAIDIIYSLITSCHNSKRMIDIAIQV	287
Db	236	FKAHMGQKHRAMRVFAVWLFIELLCWLPYNLVLLADTLMTQVIOQTCERRNHINRALDA	295
Qy	288	TESTALFHSCNLNLLYVFMGASFNKYVMKAKYKGSWRQRQSVSEFFPDSD	338
Db	296	TEILGIUHSCLNPLIYAFIQKPRHGLLKTALING-----LISKDSLKPDSD	341

Search completed: August 6, 2002, 18:09:48
Job time: 138 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 17:57:40 ; Search time 32.78 Seconds
(without alignments)
1185.962 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEQNQSTDYIYENEMNG.....VEEFPDSEGTPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	20	AA1980
2	1819	100.0	350	20	AA1981
3	1819	100.0	350	20	AA1982
4	1819	100.0	350	20	AA1983
5	1819	100.0	350	20	AA1984
6	1819	100.0	350	20	AA1985
7	1819	100.0	350	20	AA1986
8	1819	100.0	350	20	AA1987
9	1814	99.7	349	20	AA1988
10	1814	99.7	350	20	AA1989
11	1810	99.5	350	21	AA1990

12	1810	99.5	350	21	AA1980
13	1808	99.4	350	21	AA1981
14	1728	95.0	333	20	AA1982
15	1620	89.1	350	22	AA1983
16	1591	87.5	350	20	AA1984
17	1275	70.1	246	20	AA1985
18	1257	69.1	242	22	AA1986
19	1212	66.6	263	20	AA1987
20	862	47.4	164	22	AA1988
21	862	47.4	164	22	AA1989
22	824	45.3	159	21	AA1990
23	761	41.8	175	22	AA1991
24	761	41.8	175	22	AA1992
25	761	41.8	175	22	AA1993
26	761	41.8	175	22	AA1994
27	761	41.8	175	22	AA1995
28	761	41.8	175	22	AA1996
29	659	36.2	358	15	AA1997
30	659	36.2	358	21	AA1998
31	659	36.2	378	19	AA1999
32	659	36.2	378	21	AA2000
33	659	36.2	378	22	AA2001
34	659	36.2	378	22	AA2002
35	659	36.2	410	15	AA2003
36	659	36.2	410	19	AA2004
37	659	36.2	410	21	AA2005
38	659	36.2	569	22	AA2006
39	656	36.1	378	15	AA2007
40	655	36.0	378	21	AA2008
41	653	35.9	378	21	AA2009
42	650	35.7	378	21	AA2010
43	643	35.3	369	22	AA2011
44	643	35.3	378	15	AA2012
45	643	35.3	378	19	AA2013

ALIGNMENTS

RESULT 1

AA1980
ID AA1980 standard; Protein: 350 AA.

AC AA1980;

DT 05-JUN-2000 (first entry)

DE Human BGCR protein.

OS BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.

OS Homo sapiens.

PN WO9952945-A2.

PD 21-OCT-1999.

PF 16-APR-1999; 99WO-US08395.

PR 16-APR-1998; 98US-0061753.

PR 16-APR-1999; 99US-0061753.

(MILL-) MILLENNIUM PHARM INC.

Gonzalo JA, Gutierrez-Ramos JC;

WPI: 1999-620375/53.

N-PSDB; AA290528.

New nucleic acid encoding human BGCR receptor, used e.g. for modulating inflammation and tumor growth

```
XX PS Claim 8; Fig 2A-B; 123pp; English.
XX CC The invention relates to a human BGCKr protein, a G-protein coupled
XX CC receptor. The BGCKr protein can be expressed by standard recombinant
XX CC methodology. BGCKr are receptor proteins possibly involved in modulation
XX CC of proinflammatory or stimulatory functions of chemokines; cell
XX CC proliferation, migration, adhesion and targeting, and exocytosis. The
XX CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
XX CC and modulators are potentially useful for modulating inflammation;
XX CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
XX CC tumour growth; allergic reactions and entry of human immune deficiency
XX CC virus into cells, for therapeutic or prophylactic purposes. They are also
XX CC used for diagnosis and in drug-screening assays. The present sequence
XX CC represents the full-length human BGCKr protein.
XX SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSTDYEEENMGTYDYQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 1 maleqngstdyeeenmgtydysqyellicikedvrefakvflpvfltlvfviglagns 60
QY 61 MVVAIYAYKKQRTDVIYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 mvvaiyaykkqrtdviylnlavaddlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 lnfvsqmqflacisidryavatkvpqsogvgkpcwiicfcvwmaaillspqlvftvnd 180
QY 181 NARCIPFPRLYGTSMKALIQMLEICIGFVVPFLMGVCFYFARTLMKMPNIIKISRPLK 240
DB 181 narcipfprlygtsmkaliqmlaicigfvpvflmgvcyfartlmkmpniiakisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYVKFCRAIDIIYSLITSCNMKRMIDIAIOVTESIALFHSCNLP 300
DB 241 vlltvvifvltqlpyniyvkfcradiliiyslitscnmkrmidiaiovtesialfhscnlp 300
QY 301 ILVFMGASFKNYVMKAKKYGSRWRQQRQSVVEEFPDSEGPTEPTSTFSI 350
DB 301 ilvfmgasfknymkakygswrrqrsveefpdsgeptstfsi 350

RESULT 2
AA17435
ID AA17435 standard; Protein; 350 AA.
XX AC AA17435;
XX DT 29-JUL-1999 (first entry)
XX DE Human signal peptide-containing protein SP-16.
XX KW Human; signal peptide-containing protein; SP; cell proliferation;
XX KW cancer; neuronal disorder; immune response; detection.
XX OS Homo sapiens.
XX PN W09924463-A2.
XX PD 20-MAY-1999.
XX PF 04-NOV-1998; 98WO-US23578.
XX PR 07-NOV-1997; 97US-0966316.
XX PA (INCY-) INCYTE PHARM INC.
XX OS Homo sapiens.

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
XX WPI; 1999-337694/28.
XX N-PSDB; AAX61288.
XX CDNA clones encoding signal peptide-containing proteins
XX Claim 1; Fig 1; 83pp; English.
XX The present sequence represents a human signal peptide-containing
XX CC protein (SP), designated SP-16. SP proteins can be used to stimulate
XX CC cell proliferation or to treat or prevent cancer. SP antagonists are
XX CC also used to treat or prevent cancer, and also for treating or
XX CC preventing neuronal disorders or immune responses. Polynucleotide
XX CC sequences complementary to the SP-encoding polynucleotides are useful
XX CC for the detection of SP-encoding nucleic acid molecules in biological
XX CC samples.
XX SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSTDYEEENMGTYDYQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 1 maleqngstdyeeenmgtydysqyellicikedvrefakvflpvfltlvfviglagns 60
QY 61 MVVAIYAYKKQRTDVIYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 mvvaiyaykkqrtdviylnlavaddlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 lnfvsqmqflacisidryavatkvpqsogvgkpcwiicfcvwmaaillspqlvftvnd 180
QY 181 NARCIPFPRLYGTSMKALIQMLEICIGFVVPFLMGVCFYFARTLMKMPNIIKISRPLK 240
DB 181 narcipfprlygtsmkaliqmlaicigfvpvflmgvcyfartlmkmpniiakisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYVKFCRAIDIIYSLITSCNMKRMIDIAIOVTESIALFHSCNLP 300
DB 241 vlltvvifvltqlpyniyvkfcradiliiyslitscnmkrmidiaiovtesialfhscnlp 300
QY 301 ILVFMGASFKNYVMKAKKYGSRWRQQRQSVVEEFPDSEGPTEPTSTFSI 350
DB 301 ilvfmgasfknymkakygswrrqrsveefpdsgeptstfsi 350

RESULT 3
AAW93169
ID AAW93169 standard; Protein; 350 AA.
XX AC AAW93169;
XX DT 24-MAY-1999 (first entry)
XX DE Human HETA041 protein.
XX KW HETA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
XX KW treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2;
XX KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
XX KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
XX KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
XX KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
XX KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
XX KW anxiety; manic depression; delirium; dementia; severe mental retardation;
XX KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
XX KW linkage analysis; gene mapping; human.
XX OS Homo sapiens.
```

PN EP899332-A2.
XX 03-MAR-1999.
XX 17-FEB-1998; 98EP-0301170.
XX 27-OCT-1997; 97US-0962922.
PR 15-AUG-1997; 97US-0055895.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Ellis CE;
XX WPI; 1999-144803/13.
DR N-PSDB; AAX22557.
XX New G-coupled receptor (HFA041) polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease
XX
PS Claim 1; Page 22-23; 27pp; English.
XX
CC This sequence represents a G-coupled receptor, HFA041 which is useful
CC for diagnosing susceptibility to diseases by detecting mutations in the
CC HFA041 gene, and can diagnose diseases associated with HFA041 protein
CC imbalance by determining HFA041 polypeptide expression levels. Agonists
CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) HFA041 activity, in addition to direct
CC administration of antisense sequences to prevent expression, or HFA041
CC polynucleotides to treat conditions associated with a lack of HFA041
CC protein. Gene therapy may also be used to affect endogenous HFA041
CC polypeptide expression. HFA041 antibodies are useful for inducing an
CC immune response to immunise and prevent disease, and for isolating
CC HFA041 clones or purifying the polypeptides by affinity chromatography.
CC HFA041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergies; benign prostatic hypertrophy; and psychoticic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC HFA041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.
XX
SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEONQSTDYIYENENMGTYDSQYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
Db 1 maleqnqstdyvyeenmgtydsqyelickedvrefakvflpvfltvfviglagns 60

Qy 61 MVVATYAYKKQRTKTDVYIINLAVADLLLTLPFWAVNAVHGVGLCKIMCKITSALYT 120
Db 61 mvvalyaykkqrkttdvyiinlavadllltlpfwavnavhgvglckimckitsalyt 120

Qy 121 LNFVSGMFLACISIDRYVAVTKVPSQSGVKGPCWIIICFVMMAAILLISIPOLVFYTVND 180
Db 121 lnfvsqgmflacisidryvavtkvpsqsgvkpcwiiicfvmmaaillispqlvfytvnd 180

Qy 181 NARCIPFPRIYLGTSNKAQIOMLEICIGFVFPFLMGVCYFITATLKMKNPKISRLPK 240
Db 181 narcipifprrylgtsmkaligmlaicigfvpvflmgvcyfitatlmkmpniklsrplk 240

Qy 241 VLLTVVIVFTQLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIQVTFESIALFHSCLNP 300
Db 241 vlltvvfvftqlpynivkvfcraidiilyslitscnmskrmdiaiqvtesialfhscinp 300

Qy 301 ILYVFMGASFKNYVMKVAKKYGSRQRQSVVEFPFDSGPTPTSTFSI 350
Db 301 ilyvfmgsfknymkvakkygswrrqrqsvvefpfdsegptstfsi 350

RESULT 4
AAY94325
ID AAY94325 standard; Protein; 350 AA.
XX
AC AAY94325;
XX
DT 11-AUG-2000 (first entry)
XX
DE Human seven transmembrane receptor VSHK-1.
XX
KW Human; seven transmembrane receptor; VSHK-1; signal transduction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6..8
FT Modified-site /note= "potential N-glycosylation site"
FT Modified-site 19..21
FT Domain /note= "potential N-glycosylation site"
FT Domain 42..66
FT Domain /label= Transmembrane_domain
FT Domain 79..100
FT Domain /label= Transmembrane_domain
FT Domain 114..135
FT Domain /label= Transmembrane_domain
FT Domain 156..175
FT Domain /label= Transmembrane_domain
FT Domain 199..221
FT Domain /label= Transmembrane_domain
FT Domain 241..262
FT Modified-site 276..278
FT Domain /note= "potential N-glycosylation site"
FT Domain 287..308
FT Domain /label= Transmembrane_domain
XX
PN WO200026369-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-US25848.
XX
PR 04-NOV-1998; 98US-0107112.
PR 06-JAN-1999; 99US-0114856.
XX
PA (CHIR) CHIRON CORP.
XX
PI Khoja H, Shymala V;
XX
DR WPI; 2000-365618/31.
DR N-PSDB; AAY94325.
XX
PT Novel polypeptide comprising a new seven-transmembrane receptor protein
XX and its encoding polynucleotide, useful for the analysis of VSHK-1 -
PS Claim 3; Fig 1; 79pp; English.
XX
CC The present sequence is VSHK-1, a new seven transmembrane
CC receptor which contains seven membrane-spanning helical domains
CC that are linked by three intracellular and three extracellular loops. The
CC gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart
CC tissue, where VSHK-1 is predominantly found, three RNA species were
CC identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide
CC encoding the present sequence corresponds to the 2.0kb form. The 1.3kb
CC form may result from the use of an alternative polyadenylation site while
CC transcription of a 3.0kb intron at nucleotide 74 could account for the
CC 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes

CC to detect and measure VSHK-1 mRNA. They may also be used to identify
CC substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding
CC sequence can be integrated into an expression vector for production of
CC VSHK-1 receptor polypeptides in host cells. The polypeptides can be used
CC to identify agents which modulate VSHK-1 receptor signal transduction
CC activity.
XX
SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 21; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEQNSQTDYYEENEMNGTYDSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNS 60
Db 1 maleqnsqtdyyeenemngtydsqyelickedvrefakvflpvlftivfiviglagns 60

Qy 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db 61 mvvaiyaykkqrtktdivyilnlavadlllftlpfwavnavhgvlgkimckitsalyt 120

Qy 121 LNFVSGMFLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPOLVFTVND 180
Db 121 lnfvsgmflacisidryavtkvpqsgvgkpcwiiicfcvwwmaailisipqlvftvnd 180

Qy 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
Db 181 narcipiprlylgtsmkallqleicigfvpflmgvcyfitartlmkmpnikisrplk 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESTIALFHSCLNP 300
Db 241 vlltvvivfivtqlpynivkfcraidiyslitscnmskrmdiaiqvtesialfhsclnp 300

Qy 301 ILVFMGASFKNYVMKAKYGSWRQRQSVVEFPDSEGPTEPTSTFSI 350
Db 301 ilvfmgasfknymkvakkygswrrqrqsvveefpdsgeptstfsi 350

RESULT 5
AAG80119
ID AAG80119 standard; Protein; 350 AA.
XX
AC AAG80119;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CRI1 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP03708.
XX
PR 31-MAR-2000; 2000DE-1016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
XX WPI; 2001-626256/72.
XX
DR Diagnostic agent containing two or more receptor-specific ligands,
PT

PT useful for detecting tumors, inflammation etc., also therapeutic use of
PT ligand inhibitors -
XX
PS Disclosure; Page 11; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention.
XX
SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEQNSQTDYYEENEMNGTYDSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNS 60
Db 1 maleqnsqtdyyeenemngtydsqyelickedvrefakvflpvlftivfiviglagns 60

Qy 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db 61 mvvaiyaykkqrtktdivyilnlavadlllftlpfwavnavhgvlgkimckitsalyt 120

Qy 121 LNFVSGMFLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPOLVFTVND 180
Db 121 lnfvsgmflacisidryavtkvpqsgvgkpcwiiicfcvwwmaailisipqlvftvnd 180

Qy 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
Db 181 narcipiprlylgtsmkallqleicigfvpflmgvcyfitartlmkmpnikisrplk 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESTIALFHSCLNP 300
Db 241 vlltvvivfivtqlpynivkfcraidiyslitscnmskrmdiaiqvtesialfhsclnp 300

Qy 301 ILVFMGASFKNYVMKAKYGSWRQRQSVVEFPDSEGPTEPTSTFSI 350
Db 301 ilvfmgasfknymkvakkygswrrqrqsvveefpdsgeptstfsi 350

RESULT 6
AAU08994
ID AAU08994 standard; Protein; 350 AA.
XX
AC AAU08994;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human G protein-coupled receptor, GPCR, 2398.
XX
KW Human; GPCR; G protein-coupled receptor; 2398; cardiant;
KW antiatherosclerotic; analgesic; cytostatic; antianginal;
KW cardiovascular disorder; angiogenesis-related disorder;
KW neural disorder; pain response disorder; inflammatory disorder;
KW atherosclerosis; angina pectoris; myocardial infarction;
KW ischaemic heart disease; sudden cardiac death; obesity;
KW hypertensive heart disease; diabetes; prostate cancer-related pain.
XX
OS Homo sapiens.

```
XX FH Key Location/Qualifiers
FT Region 125..141
FT /label= G_protein_receptor_signature
XX WO2000164882-A2.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US06543.
XX 29-FEB-2000; 2000US-186059P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Galvin KM, Sillos-Santiago I;
XX WPI; 2001-589866/66.
XX N-PSDB; AAS14572.
XX Novel G protein coupled receptors and nucleic acids encoding them, for
XX identifying agents for the treatment of cardiac disorders -
XX Claim 9; Fig 9; 209pp; English.
XX The invention relates to novel human G protein-coupled receptors (GPCR)
XX named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and
XX nucleic acids encoding them are useful for identifying agents for the
XX treatment of cardiovascular disorders, angiogenesis-related disorders,
XX neural disorders, pain response disorders and inflammatory disorders
XX e.g. atherosclerosis, angina pectoris and myocardial infarction,
XX ischaemic heart disease, sudden cardiac death, hypertensive heart
XX disease, diabetes, prostate cancer-related pain, diabetes and obesity.
XX The present sequence represents GPCR 2398.
XX Sequence 350 AA;
XX
XX Query Match 100.0%; Score 1819; DB 22; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-195;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEQNQSTDYEEENMGTYDYSQYELICIKEDVREFAKVPFLPVLTIVFVIGLAGNS 60
Db 1 maleqnqstdyeeenmgtydsqyelickedvrefakvflpvlftivfvgiagns 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 mvvaiyaykkrtkttdvyilnlavadlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsgmqflacisidryvavtkvpqsgvgkpcwliicfcvwmaaillslpqlvftvnd 180
QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
Db 181 narcipfprylgtsmkaligleicigfvpflmgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVQLPNYIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
Db 241 vllttvvivfivqlpnyivkfcraidllyslitscnmskrmidiaiqvtesialfhsclnp 300
QY 301 ILIYFMGASFKNYMKVAKKYGSWRRQSQVEEFPDSEGPTEPTSTFSI 350
Db 301 iliyvmgasfknymkvakkygswrrqsqveefpfdsegppteptstfsi 350
XX
RESULT 7
AAG67237
ID AAG67237 standard; Protein; 350 AA.
XX
AC AAG67237;
XX
```

```
DT 13-NOV-2001 (first entry)
XX Amino acid sequence of human chemokine receptor CCR11.
XX Human; chemokine receptor; CCR11; G protein coupled receptor;
XX inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
XX asthma; angiogenesis; atherosclerosis vascular association disease;
XX hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
XX left ventricular diastolic dysfunction;migraine; preterm labour;
XX oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
XX myocardial infarction; congestive heart failure; endometriosis;
XX vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
XX Homo sapiens.
XX WO200166598-A2.
XX 13-SEP-2001.
XX 05-MAR-2001; 2001WO-US07073.
XX 03-MAR-2000; 2000US-0186928.
XX 03-MAR-2000; 2000US-0187231.
XX (ICOS-) ICOS CORP.
XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
XX WPI; 2001-541918/60.
XX N-PSDB; AAH77711.
XX An isolated polynucleotide encoding the chemokine receptor CCR11,
XX useful for treating rheumatoid arthritis, inflammatory bowel disease,
XX asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
XX phenomenon and migraine -
XX Claim 13; Page 96-97; 110pp; English.
XX
XX The present sequence represents the human chemokine receptor CCR11.
XX CCR11 is a member of the G protein coupled receptor family. A CCR11
XX polypeptide, its inhibitor, an antibody, or other modulator of CCR11
XX expression or biological activity, is useful for treating many
XX inflammatory diseases, for example, rheumatoid arthritis, inflammatory
XX bowel disease, and asthma. They are also useful for treating
XX angiogenesis, atherosclerosis vascular association diseases which may
XX include but are not limited to hypertension, angina pectoris, cardiac
XX arrhythmias, left ventricular diastolic dysfunction, Raynaud's
XX phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
XX stroke, subarachnoid haemorrhage, myocardial infarction, congestive
XX heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
XX pulmonary vascular disease.
XX Sequence 350 AA;
XX
XX Query Match 100.0%; Score 1819; DB 22; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-195;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEQNQSTDYEEENMGTYDYSQYELICIKEDVREFAKVPFLPVLTIVFVIGLAGNS 60
Db 1 maleqnqstdyeeenmgtydsqyelickedvrefakvflpvlftivfvgiagns 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 mvvaiyaykkrtkttdvyilnlavadlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsgmqflacisidryvavtkvpqsgvgkpcwliicfcvwmaaillslpqlvftvnd 180
QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
XX
```

Db 181 narcipfprylgtsmkaligmlcigfvpflimgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMKRMEDIAIQVTSIALFHSLNP 300
Db 241 vlltvvfvivtqlpynivkfcraidiyslitscnmskrmdiaiqvtsialfhslnp 300
QY 301 ILYVFMGASFKNYVMKVKYGSRRQRQSVVEFPDSEGPTPTSTFSI 350
Db 301 illyvfmgasfknymkvakkygswrrqrqsvvefpdsegptptstfsi 350

RESULT 8
AAB62389
ID AAB62389 standard; Protein; 382 AA.
AC AAB62389;
XX
DT 29-JUN-2001 (first entry)
DE Human chemokine receptor CCX CKR polypeptide.
KW Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator;
KW antinflammatory; immunosuppressive; cytostatic; antiallergic; human;
KW immunostimulant; gene therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 351 /note= "encoded by TAA"
FT Misc-difference 353 /note= "encoded by TAA"
FT Misc-difference 365 /note= "encoded by TGA"
FT Misc-difference 371 /note= "encoded by TAA"
XX
PN WO200127146-A2.
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-US28067.
PR 12-OCT-1999; 99US-0159015.
PR 13-OCT-1999; 99US-0159210.
PR 20-DEC-1999; 99US-0172979.
PR 28-DEC-1999; 99US-0173389.
PR 03-MAR-2000; 2000US-0186626.
XX (CHEM-) CHEMOCENTRIX INC.
PA Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
PI WPI; 2001-281975/29.
DR N-PSDB; AAF57685.
XX
PT Isolated or recombinant chemokine receptor (designated CCX CKR)
PT polypeptide (p1) or its fragment, useful for identifying CCX CKR
PT modulators which can be used in the treatment of inflammation, allergy,
PT an autoimmune disease or cancer -
XX
PS Claim 4; Fig 1; 72pp; English.
XX
CC The invention relates to an isolated or recombinant chemokine receptor
CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,
CC SLC or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR
CC modulators. An agent that modulates the activity or expression of CCX CKR
CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR
CC -mediated condition such as inflammation, allergy, an autoimmune disease,
CC graft rejection, cancer, an infectious disease or an immunosuppressive
CC disease. The present sequence represents the human CCX CKR polypeptide.
XX
SQ Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 22; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEQNSTDYDYEEENMGNTYDYSQELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60
Db 1 maleqngstddyeeenmgntdydsqelickedvrefakvlpvltivfvglagns 60
QY 61 MVVAIYAYVKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWLGKIMCKITTSALYT 120
Db 61 mvvaiyaykkrtdvylnlavadllllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYVAVTKVPVPSGSGVKPCWICFCVWMAAILLSIPQLVFFVYVND 180
Db 121 lnfvsgmqflacisidryvavtkvpvpsgsgvgkcwlcfcvwmiaalilspqlvffvtynd 180
QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
Db 181 narcipfprylgtsmkaligmlcigfvpflimgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMKRMEDIAIQVTSIALFHSLNP 300
Db 241 vlltvvfvivtqlpynivkfcraidiyslitscnmskrmdiaiqvtsialfhslnp 300
QY 301 ILYVFMGASFKNYVMKVKYGSRRQRQSVVEFPDSEGPTPTSTFSI 350
Db 301 illyvfmgasfknymkvakkygswrrqrqsvvefpdsegptptstfsi 350

RESULT 9
AAW93170
ID AAW93170 standard; Protein; 349 AA.
XX
AC AAW93170;
XX
DT 24-MAY-1999 (first entry)
DE Human HFIAO41 protein.
XX
KW HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
KW anxiety; manic depression; delirium; dementia; severe mental retardation;
KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
KW linkage analysis; gene mapping; human; ss.
XX
OS Homo sapiens.
XX
PN EP8999332-A2.
XX
PD 03-MAR-1999.
XX
PF 17-FEB-1998; 98EP-0301170.
XX
PR 27-OCT-1997; 97US-0962922.
PR 15-AUG-1997; 97US-0055895.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Ellis CE;
XX
DR WPI; 1999-144803/13.
DR N-PSDB; AAX22558.
XX
PT New G-coupled receptor (HFIAO41) polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease

XX PS Disclosure; Page 25-26; 27pp; English.

XX CC This sequence encodes a G-coupled receptor, HFAO41 which is useful for

XX CC diagnosing susceptibility to diseases by detecting mutations in the

XX CC HFAO41 gene, and can diagnose diseases associated with HFAO41 protein

XX CC imbalance by determining HFAO41 polypeptide expression levels. Agonists

XX CC and antagonists of the protein can be used in treatment to activate

XX CC (agonist) or inhibit (antagonist) HFAO41 activity, in addition to direct

XX CC administration of antisense sequences to prevent expression, or HFAO41

XX CC polynucleotides to treat conditions associated with a lack of HFAO41

XX CC protein. Gene therapy may also be used to affect endogenous HFAO41

XX CC polypeptide expression. HFAO41 antibodies are useful for inducing an

XX CC immune response to immunize and prevent disease, and for isolating

XX CC HFAO41 clones or purifying the polypeptides by affinity chromatography.

XX CC HFAO41 polypeptides can be administered directly or as a vaccine to

XX CC inoculate against disease. Diseases diagnosed, prevented and treated

XX CC include bacterial, fungal, protozoan and viral infections, particularly

XX CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's

XX CC disease; acute heart failure; hypotension; hypertension; urinary

XX CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;

XX CC asthma; allergies; benign prostatic hypertrophy; and psychotic and

XX CC neurological disorders, including anxiety, schizophrenia, manic

XX CC depression, delirium, dementia, severe mental retardation and dyskinesias

XX CC such as Huntington's disease or Gilles de la Tourette's syndrome. The

XX CC HFAO41 polypeptide is also useful for mapping the gene to a chromosome,

XX CC allowing gene inheritance to be studied through linkage analysis.

XX SQ Sequence 349 AA;

Query Match 99.7%; Score 1814; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 5.8e-195;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPLPVLFIIVFVIGLAGNSM 61
DB 1 ALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPLPVLFIIVFVIGLAGNSM 60

QY 62 VVAIVAYYKKORTKTDVYILNLAVALDLELFTLPFWAVNAVHGVLGIMCKITISALYTL 121
DB 61 VVAIVAYYKKORTKTDVYILNLAVALDLELFTLPFWAVNAVHGVLGIMCKITISALYTL 120

QY 122 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVNDN 181
DB 121 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVNDN 180

QY 182 ARCPIFPFRLYIGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 241
DB 181 ARCPIFPFRLYIGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240

QY 242 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 301
DB 241 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300

QY 302 LYVFMGASFKNYVMKVAKYGSWRQRORSVEEFPDSEGPTEPTSTFSI 350
DB 301 LYVFMGASFKNYVMKVAKYGSWRQRORSVEEFPDSEGPTEPTSTFSI 349

RESULT 10
AAV30125
ID AAV30125 standard; Protein; 350 AA.
XX AC AAV30125;
XX DT 14-OCT-1999 (first entry)
XX DE A human seven-pass transmembrane receptor protein.
XX KW Seven-pass transmembrane receptor; autoimmune disease;
XX KW white blood cell dysfunction.

OS Homo sapiens.
XX PN WO9933876-A1.
XX PD 08-JUL-1999.
XX PF 24-DEC-1998; 98WO-JP05886.
XX PR 24-DEC-1997; 97JP-0354537.
XX PA (ASAH) ASAH KASEI KOGYO KK.
XX PI Ishimaru H, Koshio T, Ohno T;
XX DR WPI; 1999-493806/41.
XX DR N-PSDB; AAX86674.
XX PT New seven-pass transmembrane receptor protein useful for treating,
XX PT preventing or diagnosing autoimmune diseases
XX PS Claim 1; Page 101-103; 118pp; Japanese.
XX CC The present sequence represents a seven-pass transmembrane receptor
XX CC protein. The protein and its DNA can be used to screen substances
XX CC for the diagnosis, prevention and treatment of autoimmune diseases,
XX CC particularly those due to white blood cell dysfunction.

SQ Sequence 350 AA;

Query Match 99.7%; Score 1814; DB 20; Length 350;
Best Local Similarity 99.7%; Pred. No. 5.8e-195;
Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPLPVLFIIVFVIGLAGNS 60
DB 1 MALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPLPVLFIIVFVIGLAGNS 60

QY 61 MVVAIVAYYKKORTKTDVYILNLAVALDLELFTLPFWAVNAVHGVLGIMCKITISALYTL 120
DB 61 MVVAIVAYYKKORTKTDVYILNLAVALDLELFTLPFWAVNAVHGVLGIMCKITISALYTL 120

QY 121 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180

QY 181 NARCPIFPFRLYIGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240
DB 181 NARCPIFPFRLYIGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240

QY 241 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300
DB 241 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300

QY 301 ILYVFMGASFKNYVMKVAKYGSWRQRORSVEEFPDSEGPTEPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKVAKYGSWRQRORSVEEFPDSEGPTEPTSTFSI 350

RESULT 11
AAV71301
ID AAV71301 standard; Protein; 350 AA.
XX AC AAV71301;
XX DT 02-NOV-2000 (first entry)
XX DE Human orphan G protein-coupled receptor hPPR1.
XX KW Human; orphan G protein-coupled receptor; GPCR; hPPR1; drug screening;
XX KW transmembrane receptor; expressed sequence tag; EST; signal cascade.

OS Homo sapiens.

PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents -
PS Example 1; Page 99-100; 187pp; English.
XX
XX
XX The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
XX

SQ Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;
Best Local Similarity 99.4%; Pred. No. 1.6e-194;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MALEQNQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Db 1 maleqnqstdyveenemngtydysqyelickedvrefakvflpvfltiafviglagns 60
Qy 61 MVVAIYAYKKORTDVIILNAVADLLLTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db 61 mvvaiyaykkqrtkdviilnavadlllftlpfwavnavhgvlgkimckitsalyt 120
Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsqmqflacisidryvavtnvpsqsgvqkpcwiiicfcvwwmaailisipqlvftvnd 180
Qy 181 NARCIPPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIIKISRPLK 240
Db 181 narcipifprylgtsmkaligmeicigfvpflmgvcyftartlmkmpnikisrplk 240
Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
Db 241 vlltvvifvtqlpynivkfcraidiislylitscnmskrmdiaiqvtesialfhsclnp 300
Qy 301 ILIYPMGASFKNYVMKAKKYGSRQRQSVSEFFPDSGTEPTSTFSI 350
Db 301 illyvmgasfknyvmkakygswrrqrqsvseefpdsgeptstfsi 350

RESULT 13

AAB37788
ID AAB37788 standard; Protein: 350 AA.

XX AAB37788;

XX 23-FEB-2001 (first entry)

XX Human TSC7.

XX Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial;
KW osteopathic; antiulcer; antiasthmatic; antiallergic; neuroprotective;
KW cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;
KW analgesic; tranquilizer; immunosuppressive; antiinflammatory;
KW gene therapy; TSC7; infection; cancer; autoimmune disorder;
KW Parkinson's disease; osteoporosis; neurological disorder.
XX

OS Homo sapiens.

XX WO2000064941-A2.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10979.

XX 23-APR-1999; 99US-0130817.

PR 20-APR-2000; 2000US-0556002.
XX (CURA-) CURAGEN CORP.
XX
XX Gould-Rothberg BE;
XX
XX WPI; 2000-679670/66.
DR N-PSDB; AAC68722.
XX
XX Novel nucleic acid encoding G-protein coupled receptor for diagnosis
PT and treatment of conditions associated with disorder in a G-protein
PT mediated pathway such as cancer, neurological disorders and infections
XX
XX Claim 12; Page 8; 132pp; English.

XX The present sequence is human tuberous sclerosis complex 7 (TSC7).
CC TSC7 polynucleotides and polypeptides are useful for determining the
CC presence or predisposition to a disease associated with altered levels of
CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the
CC polypeptide are useful for treating or preventing pathological conditions
CC associated with the disorder in a G-protein mediated pathway. They are
CC useful for diagnosing a hyperproliferative condition such as a neoplasm
CC or dermatological condition. TSC7 nucleic acids and polypeptides are
CC useful in the treatment of microbial infections, pain, cancer, anorexia,
CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,
CC hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy
CC and psychotic and neurological disorders, including schizophrenia,
CC dementia, severe mental retardation and dyskinesias, such as
CC Huntington's disease and/or other pathologies and disorders. TSC7
CC polypeptides are also useful as immunogens to produce antibodies and as
XX vaccines.

SQ Sequence 350 AA;

Query Match 99.4%; Score 1808; DB 21; Length 350;
Best Local Similarity 99.4%; Pred. No. 2.7e-194;
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALEQNQSTDYVEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Db 1 maleqnqstdyveenemngtydysqyelickedvrefakvflpvfltivfiviglagns 60
Qy 61 MVVAIYAYKKORTDVIILNAVADLLLTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db 61 mvvaiyaykkqrtkdviilnavadlllftlpfwavnavhgvlgkimckitsalyt 120
Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsqmqflacisidryvavtnvpsqsgvqkpcwiiicfcvwwmaailisipqlvftvnd 180
Qy 181 NARCIPPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIIKISRPLK 240
Db 181 narcipifprylgtsmkaligmeicigfvpflmgvcyftartlmkmpnikisrplk 240
Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
Db 241 vlltvvifvtqlpynivkfcraidiislylitscnmskrmdiaiqvtesialfhsclnp 300
Qy 301 ILIYPMGASFKNYVMKAKKYGSRQRQSVSEFFPDSGTEPTSTFSI 350
Db 301 illyvmgasfknyvmkakygswrrqrqsvseefpdsgeptstfsi 350

RESULT 14

AAV57289
ID AAV57289 standard; Protein: 333 AA.

XX AAV57289;

XX 05-JUN-2000 (first entry)

```
XX DE Human BGCR partial amino acid sequence.
XX
XX BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX
XX Homo sapiens.
OS
XX WO9952945-A2.
XX
XX 21-OCT-1999.
XX
XX 16-APR-1999; 99WO-US08395.
XX
XX 16-APR-1998; 98US-0061753.
XX
XX 16-APR-1999; 99US-0061753.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX Gonzalo JA, Gutierrez-Ramos JC;
PI
XX WPI; 1999-620375/53.
XX
XX N-PSDB; AAZ90527.
DR
XX
XX New nucleic acid encoding human BGCR receptor, used e.g. for
PT modulating inflammation and tumor growth
PT
XX
XX Claim 1; Fig 1A-B; 123pp; English.
PS
XX The invention relates to a human BGCR protein, a G-protein coupled
CC receptor. The BGCR protein can be expressed by standard recombinant
CC methodology. BGCR are receptor proteins possibly involved in modulation
CC of proinflammatory or stimulatory functions of chemokines; cell
CC proliferation, migration, adhesion and targeting, and exocytosis. The
CC BGCR nucleic acids and derived proteins (or their variants), antibodies
CC and modulators are potentially useful for modulating inflammation;
CC chemotactant activity of leucocytes; angiogenesis; cell proliferation;
CC tumour growth; allergic reactions and entry of human immune deficiency
CC virus into cells, for therapeutic or prophylactic purposes. They are also
CC used for diagnosis and in drug-screening assays. The present sequence
CC represents the sequence of a partial human BGCR protein.
XX
XX Sequence 333 AA;
SQ
Query Match 95.0%; Score 1728; DB 20; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.5e-185;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 MNGTYDYSQVELICIKEDVREFAKVLPVFTIVFVIGLAGNSMVVAIYAYKKQRTKTD 77
DB 1 mngtydysqvelicikedvrefakvlpvftivfiviglagnsmvvaiyaykkqrktkd 60
QY 78 VYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYTLNFSVGMQFLACISIDR 137
DB 61 vyilnlavaddlllftlpfwavnavhgwlgkimckitsalyltnfsvgmqflacisidr 120
QY 138 YVAVTKVPSSGVGKPCWICFCVWMAAILLSIPQLVFTVNDNARCIPIFPRLYGTSMK 197
DB 121 yvavtkvpssgv9gkpcwlcfcvwmaailslpqlvftvndnarcipifprylgtsmk 180
QY 198 ALIOMLEICIGFVVPFLIMGVCVFITARTLMKMPNLIKISRLPKVLLPVIIVTQLPYN 257
DB 181 aliqlmleicigfvvpflimgvcvfitartlmkmpnikisrplkvlltwivfvtqlpyn 240
QY 258 IVKFCRAIDIIYSLITSCNMSKMDIAOVTESALPHSCINPLTYVFMGSFKNYVMKV 317
DB 241 ivkfcraidl iyslitscnmskmdiaqvtesialfhsclnpltyvfmgsfknymkv 300
QY 318 AKKYGSRQRQSVSEEPFDSGTEPTSTFSI 350
DB 301 akkygswrrqrqsvseefpdsgeptstfsi 333
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RESULT 15
AAG67238
ID AAG67238 standard; Protein; 350 AA.
XX
XX AAG67238;
XX
XX 13-NOV-2001 (first entry)
DT
XX Amino acid sequence of bovine chemokine receptor CCR11.
DE
XX Human; chemokine receptor; CCR11; G protein coupled receptor;
KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; arteriosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction; migraine; preterm labour;
KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosis;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
XX
XX Bos sp.
OS
XX WO200166598-A2.
XX
XX 13-SEP-2001.
XX
XX 05-MAR-2001; 2001WO-US07073.
XX
XX 03-MAR-2000; 2000US-0186928.
XX
XX 03-MAR-2000; 2000US-0187231.
XX
XX (ICOS-) ICOS CORP.
PA
XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
PI
XX WPI; 2001-541918/60.
XX
XX N-PSDB; AAH77712.
DR
XX An isolated polynucleotide encoding the chemokine receptor CCR11,
XX useful for treating rheumatoid arthritis, inflammatory bowel disease,
XX asthma, angiogenesis, arteriosclerosis, cardiac arrhythmias, Raynaud's
XX phenomenon and migraine
XX
XX Example 1; Page 99-100; 110pp; English.
XX
XX The present sequence represents the bovine chemokine receptor CCR11.
XX CCR11 is a member of the G protein coupled receptor family. A CCR11
XX polypeptide, its inhibitor, an antibody, or other modulator of CCR11
XX expression or biological activity, is useful for treating many
XX inflammatory diseases, for example, rheumatoid arthritis, inflammatory
XX bowel disease, and asthma. They are also useful for treating
XX angiogenesis, arteriosclerosis vascular association diseases which may
XX include but are not limited to hypertension, angina pectoris, cardiac
XX arrhythmias, left ventricular diastolic dysfunction, Raynaud's
XX phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
XX stroke, subarachnoid haemorrhage, myocardial infarction, congestive
XX heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
XX pulmonary vascular disease.
XX
XX Sequence 350 AA;
SQ
Query Match 89.1%; Score 1620; DB 22; Length 350;
Best Local Similarity 86.0%; Pred. No. 3.5e-173;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;
QY 1 MALQONSTDYYYENENMGTYDYSQVELICIKEDVREFAKVLPVFTIVFVIGLAGNS 60
DB 1 maveyngstdyyyenenmndthdysqvycikeevrkfakvlpafptiafiaglns 60
QY 61 MVVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALY 120
DB 1 mvvaiyaykkqrktkdvyilnlavaddlllftlpfwavnavhgwlgkimckitsalyl
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QY 181 NARCIPFPRLYLGTSKALIQMLEICIGFVFPFLINGVYCFITARTLKMKNPIKISRPLK 240
DB 181 NARCTPIFPFHHLGTSKASIQMLEIGFVFPFLINGVYCFITARTLKMKNPIKISRPLR 240
QY 241 VLLTVVIVFIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTSIALFHSCLNP 300
DB 241 VLLAVVVFIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTSIALFHSCLNP 300
QY 301 ILYVFMGASFKNVYKVAKYGSRWRQSRQSVVEFPDSEGPTEPTSTFSI 350
DB 301 ILYVFMGASFKNVYKVAKYGSRWRQSRQSVVEFPDSEGPTEPTSTFSI 350
RESULT 2
ID Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1.
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE PUTATIVE G-PROTEIN COUPLED RECEPTOR GPCR14 (FRAGMENT).
GN GPCR14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RL receptors expressed in regenerating peripheral nerve.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090348; AAG24470.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match 50.1%; Score 912; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 3.9e-73;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FVAVNAVHGVWLGKIMCKITSALYTLNFSVGMQFLACISIDRYAVATKVPQSGVGKPCW 155
DB 19 FVAVNAVHGVWILGKIMCKVTSALYTVNFVSGMFLACISIDRYAVATKVPQSGVGKPCW 78
QY 156 IICFCVMAAILLSIPQLVFNVDNARCIPFPRLYLGTSKALIQMLEICIGFVFPFLI 215
DB 79 IICCCVMTAAILLSPQLVFNVDNARCIPFPRLYLGTSKALIQMLEICIGFVFPFLI 138
QY 216 MGVCYFITARTLKMKNPIKISRPLKVLTVVIVFIVTQLPNIVKFCRAIDIIYSLTSC 275
DB 139 MGVCYAMTARKLIKMPNPKSRPLRLVAVVVFIVTQLPNIVKFCRAIDIIYSLTSC 198
QY 276 NMSKRMIDIAIQVTSIALFHSCL 298
DB 199 DMSKRMIDIAIQVTSIALFHSCL 221
RESULT 3
Q9UQ06
ID Q9UQ06 PRELIMINARY; PRT; 369 AA.
AC Q9UQ06.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

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DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RL receptor for the chemokine TECK.";
RL J. Immunol. 162:5671-5675(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RL 15).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; -
DR EMBL; AF145439; AAF66699.1; -
DR InterPro; IPR004069; Chemokine9_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 369 AA; 42015 MW; F27CEA0CFB6B44C CRC64;

Query Match 35.3%; Score 643; DB 4; Length 369;
Best Local Similarity 36.4%; Pred. No. 4.5e-49;
Matches 120; Conservative 75; Mismatches 117; Indels 18; Gaps 4;

QY 6 NQSTDYEE-NEMNGTYDYSQYELICIKEDREFAKVLPVLTIVFVIGLAGNSMVA 64
DB 12 NMADDYSESTSMEDYVNFNFTDFYCKNNVRQFASHFLPPLYLWLVFVIGLAGNSLVL 71
QY 65 IYAYYKQRTKTDVILNLAVADLLLLFLPFVAVNAVHGVWLGKIMCKITSALYTLNFV 124
DB 72 VYWTCTRVKTMDFMLLLNLAIADLLFLVLPFMAIAAADQWKFPQTFMCKVWNSYKMFY 131
QY 125 SGMQFLACISIDRYAVATKVPQSGVGKPCW-----IICFCVMAAILLSIPQLVF 175
DB 132 SCVLLIMCISVDRYATAIQ-----AMRAHTWREKRLLYSKMVCFTIWLVAALCIPEILY 186
QY 176 YTVNDN---ARCIPFPRLYLGTSKALIQMLEICIGFVFPFLINGVYCFITARTLKMKN 232
DB 187 SQIKESGIAICTMVPSPDESTKLSAVLTKVLGFFLPFVVMACCYTIIHTLIQAKK 246
QY 233 IKISRLPKVLLVIVFIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESTA 292
DB 247 SKHKALKKTIITVTLVFLVSQFPYCNILLVQTIDAYAMFISCAVSTNIDICFQVQTIA 306
QY 293 LFHSCNLPILYVFMGASFKNVYKVAKYG 322
DB 307 FPHSCNLPVLYVFGVGERFRLDKLTKNLG 336
RESULT 4
Q9R1V0
ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 9
Q9ERH5 PRELIMINARY; PRT; 351 AA.
AC Q9ERH5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN CXCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=SPLEEN;
RA Sato H., Taniguchi M.;
RT "Molecular cloning of a putative chemokine receptor preferentially
RT expressed in mouse lymphocytes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305709; AAG31284.1; -.
DR MGD; MGI:1934582; CXCR6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40511 MW; B00E3134D2B4D1ED CRC64;

Query Match 30.9%; Score 561.5; DB 11; Length 351;
Best Local Similarity 35.4%; Pred. No. 7e-42;
Matches 127; Conservative 69; Mismatches 126; Indels 37; Gaps 10;

QY 10 DYIYEN--EMGTGYDYSOYELICIKEDVR--EFAKVFLPVLFTIVFVIGLAGNSMVAI 65
DB 12 DGHYEGDFWLNSSDNSQ-----ENRFLKFEVFLPCVLYVVFVGLGSLVLI 64
QY 66 YAYKKORTDVTILNLAVADLLLTLPFWAVNAVHGWLGKIMCKITSAITYTLNFVS 125
DB 65 YIFYOKRLTDFVLNLPLADLVFCTLPFWAYAGTIEWVFGVWCKTLRGMYNFV 124
QY 126 GQFLACISIDRYAV--TKVPSOSGVGKPCW--IICFCVWMAAILSLIPQLVTVND 180
DB 125 SMLTLCITVDREIVVQATKAFNRQAKWK--IWGVICLLIIVWSLVSLPQLIYGHVD 183
QY 181 NARCIPIPRYLGTSKMKALIQMIEICIGVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
DB 184 IDKLI---CQYHSEISTMVLVIQMTGPFPLPLTLMILCYSGIITLLHARNFQKHSLK 240
QY 241 VLLTVVIVFIVTQPNVIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
DB 241 IIFLVAVFLLQTQTFNLAMLQSTSWEYITTS-----FKYIVVTEAIAIFRACLNP 294
QY 301 ILYVFMGASFKNYKVAKKYG-----SWRRQOSVEEFPDSEGTPTSTFSI 350
DB 295 VLYAFVGLKFRKNVWKLMDIGCLSHLGVSQWKSSDSK--TCSASHNVETTSMFQL 351

RESULT 10
Q9HCA5 PRELIMINARY; PRT; 342 AA.
AC Q9HCA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MUTANT G PROTEIN-COUPLED RECEPTOR STRL33.
GN STRL33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (BOB)."
RT AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=973111099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029759; AAG21918.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39279 MW; CE149633D01D20AA CRC64;

Query Match 30.8%; Score 560; DB 4; Length 342;
Best Local Similarity 33.1%; Pred. No. 9.3e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YYEENEMNGTYDYSOYELICIKEDVREFAKVFLPVLFTIVFVIGLAGNSMVAIYAYKK 71
DB 6 YHEDYGFSSFNSSQEE---HODFQFSKVFLPCVLYVVFVGLGSLVLIYISIFYHK 61
QY 72 QRTKTDVYILNLAVADLLLTLPFWAVNAVHGWLGKIMCKITSAITYTLNFVSGMOFLA 131
DB 62 LQSLTDVFLVNLPLADLVFCTLPFWAYAGIHEWVFGVWCKSLGIYITNFYTSMLILT 121
QY 132 CISIDRYAVATKVPSS--QSGVGKPCW--IICFCVWMAAILSLIPQLVTVV--NDNRCI 185
DB 122 CITVDREIVVVKATKAYNQAKRMTGWKVTSLIIVISLVSLPQLIYGNVFNLDKLCI- 180
QY 186 PIPPRYLGTSKMKALIQMIEICIGVVPFLMGVCYFITARTLMKMPNIIKISRPLKLLTV 245
DB 181 ----GVHDEAISTVLTATQMTGLFPLFMIVCYSVIIKTLHAGGFQKHSUKIIFLV 236
QY 246 VIVFIVTQPNVIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNPILYVF 305
DB 237 MAVFLLTQMPFLMKFTRSTHWEYAMTSFHYT-----IMVTEAIALRACLNPLYAF 290
QY 306 MGASFKNYKVAKKYG-----SWRRQOSVEEFPDSEGTPTSTFSI 350
DB 291 VSLKFRKNFWKLVKDIGCLPYLGVSQWKSSDSK--TFSASHNVETTSMFQL 342

RESULT 11
Q9TV16 PRELIMINARY; PRT; 342 AA.
AC Q9TV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (BOB)."
RT AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=973111099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029759; AAG21918.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39279 MW; CE149633D01D20AA CRC64;
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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match
Best Local Similarity 30.7%; Score 559; DB 6; Length 342;
Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;

QY 12 YEEENMGTYDYQYSELICIKEDVREFAKVLPLVFTIVFVIGLAGNSMVAIYAYKK 71
DB 6 YHEDYGFNSFSSQBE---HQDFLOFSKVFPLPCMYLVFVCGLVGSLVLVISIFYHK 61

QY 72 QRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTFVSGMOFLA 131
DB 62 LQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQVMCKSLGIYINFTSMILIT 121

QY 132 CISIDRYAVAVTKVPS--QSGVGKPCW--IICFCVMAAIIISIPOLVFTV--NDNARCI 185
DB 122 CITVDFIVVATRAYNOQAKRWGKVTSLIWIISLVSLPQIIYGNVFNLDKLC- 180

QY 186 PIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKPNIKISRPLKVLITV 245
DB 181 ----GYHDEAISTVVLATQMTLGFLLTMTIVCVSVIITKLLHAGGFGOKHRSKLIIFLV 236

QY 246 VIVFIVTQLPYNIIVFCRAIDIIYSLITSCNMSKRMDAIOVTESTALPHSCINPILYVF 305
DB 237 MAVFLITQMPFLNPLILIRSTHEYAYMTSFHYT-----IMVTEIAYLRACINPVLVYAF 290

QY 306 MGASEFKNYVMKAKYKG-----SWRRQSQVEEPFDEGPTPTSTFSI 350
DB 291 VSLKFKNFKWLVKDIGCLPYLGVSQHWKSSSDNSK--TFSASHNVVETASMEQL 342

RESULT 12
Q9PUA0 PRELIMINARY; PRT; 358 AA.
AC Q9PUA0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4.
GN CXCR4.
OS Acipenser ruthenus (sterlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenserinae; Acipenser.
OX NCBI_TaxID=7906;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368347; PubMed=10906389;
RA Alibayev B.I., Najashin A.M., Mechetina L.V., Tarantin A.V.;
RT "Cloning of a CXCR4 homolog in chondrosteian fish and characterization
of the CXCR4-specific structural features.";
RL Dev. Comp. Immunol. 24:765-770(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ249438; CAB60252.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40448 MW; 7B3B99B62453008 CRC64;

Query Match
Best Local Similarity 29.9%; Score 544; DB 13; Length 358;
Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;
```

```
Matches 125; Conservative 64; Mismatches 145; Indels 18; Gaps 7;

QY 8 STDYYEEN-EMNGTYDYQYSELICIKEDVREFAKVLPLVFTIVFVIGLAGNSMVAIY 66
DB 7 TVDFTFENNTGSGDYSQYDEVCKRNGLRKIFLPTVYTIIFVMGIVGSLVIVM 66

QY 67 AYYKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTFVSG 126
DB 67 G-YQKVTMTDKYRLHLLIADLLFVTLFPWADAAASSWTFGGFLCKLNNIYTNLYSS 125

QY 127 MOFLACISIDRYAVAVTKVPSQSGVKPC-----WIICFCVMAAIIISIPOLVFTVNDN 181
DB 126 VLTIAISIFSDRYLAVVRATNSH---KPKLLAEKIIYVGVWLPATLLTVPDLFVAQVHDE 182

QY 182 A---RCIPIFPYRVLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMK-MPNTKISR 237
DB 183 GTRMCDRVPYSGSGNIMWTIFRFQHFVGLVPLGLVILTCYCIITIKLSQSGSKGLQKR 242

QY 238 PLKVLTVVIVFTQLPYNIIVFCRAIDIIYSLITSCNMSKRMDAIOVTESTALPHSC 297
DB 243 ALKTTIILIAFFICWLPYCIALVDLTVLLNVIQYNCTLOHMETWIFVTEGLAYPHCC 302

QY 298 LPDILVFMGASPKNYVMKAKYKGSRRQRQSVSEFPFDEGPTPTSTFS 349
DB 303 LNSILYAFGLGVKPK----KSAKSALTVNSRSGSLKILSKNKGGLSSVSTES 350

RESULT 13
Q91ZH4 PRELIMINARY; PRT; 360 AA.
AC Q91ZH4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW;
RA Garcia G.E., Chen S., Xia Y., Harrison J., Willson C.B., Johnson R.J.,
RA Bacon K.B., Feng L.;
RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
chemokine results in attenuation of developing crescentic
glomerulonephritis.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432872; AAL30398.1; -.
KW Receptor.
SQ SEQUENCE 360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 11; Length 360;
Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;

QY 3 LEQNQSTDYYEENMGTYDYQYSELICIKEDVREFAKVLPLVFTIVFVIGLAGNSMV 62
DB 1 MNATEVTDITQDETETNSYFDESPLPKCTKEGIRAFGEVFLPPLYSLVFLGLFGNSV 60

QY 63 VAIYAYYKKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTF 122
DB 61 VLVLFKYRLKSMTDVYLLNLAISDLLFVLSLPFGWYAADQWVFLGLCKLISWMLV 120

QY 123 FVSGMOFLACISIDRYAVAVTKV-----PSQSGVGKPCWIIICFCVMAAIIISIPOLV 175
DB 121 FYSGIFIMLSIDRYLAIVHAVFSLRARTLTGV-----ITSLITWSVAVFASLPGLLF 175

QY 176 YTV---NDNARCIPIFPYRVLGTSMKALIQMLEI-CIGFVVPFLMGVCYFITARTLMKMP 231
DB 176 STCDTENNHITYCKTQYS--VNSTTWKVLSSLEINLGLVILPLGIMLFCYSMIITLRHCK 233
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:05:40 ; Search time 17.74 Seconds
(without alignments)
1895.787 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONQSTDYEEENEMNG.....VEEFPDSEGTPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	89.1	350	JN0621	G protein-coupled
2	659	36.2	378	B55735	lymphocyte-specifi
3	650	35.7	378	A55735	G protein-coupled
4	643	35.3	378	A45680	G protein-coupled
5	583	32.1	369	JC5088	G protein-coupled
6	537.5	29.5	360	A57160	chemokine (C-C) re
7	534.5	29.4	360	A53611	interleukin-8 rece
8	524	28.8	354	158186	probable G protein
9	522.5	28.7	355	JC4304	orphan G protein-c
10	522.5	28.7	360	JC4587	chemokine (C-C) re
11	518.5	28.5	354	A55733	G protein-coupled
12	511	28.1	358	A53752	interleukin-8 rece
13	501.5	27.6	355	JQ1231	interleukin-8 rece
14	500.5	27.5	352	A45747	neuropeptide Y/pep
15	499.5	27.5	353	S28787	neuropeptide Y/pep
16	493.5	27.1	352	G00048	fusin (LESTRA) - c
17	492	27.0	360	JC2443	chemokine (C-C) re
18	489.5	26.9	350	A39445	interleukin-8 rece
19	486	26.7	355	JC5067	G protein-coupled
20	485	26.7	355	T49339	macrophage inflam
21	484.5	26.6	352	A43113	chemokine (C-C) re
22	483.5	26.6	359	A48921	interleukin-8 rece
23	482	26.5	374	T38450	chemokine (C-C) re
24	479.5	26.4	359	T49341	MIP-1 alpha recept
25	476.5	26.2	367	JE0349	interferon-inducib
26	474	26.1	355	A45177	chemokine (C-C) re
27	471	25.9	356	S42096	interleukin-8 rece
28	470	25.8	383	S55594	G protein-coupled
29	461.5	25.4	355	G02436	chemokine (C-C) re

ALIGNMENTS

RESULT 1

JN0621

G Protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C:Accession: JN0621

R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A:Title: Identification of novel members of G-protein coupled receptor superfamily ex

A:Reference number: JN0621; MUID:93326166

A:Accession: JN0621

A:Molecule type: mRNA

A:Residues: 1-350 <MAT>

A:Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711

A:Experimental source: tongue taste papillae

C:Comment: This protein is involved in modulating taste sensitivity or regeneration o

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F:42-66/Domain: transmembrane #status predicted <TM1>

F:114-135/Domain: transmembrane #status predicted <TM2>

F:154-175/Domain: transmembrane #status predicted <TM3>

F:200-222/Domain: transmembrane #status predicted <TM4>

F:242-265/Domain: transmembrane #status predicted <TM5>

F:284-306/Domain: transmembrane #status predicted <TM6>

F:6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;

Best Local Similarity 86.0%; Pred. No. 1.1e-131;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALEONQSTDYEEENEMNGTYDSOYELICIKEDVREFAKVPFLPVLFTVIFVIGLAGNS 60

Db 1 MAVEYNQSTDYEEENEMNDTHDSQYEVICIKKEEFKAKVLPFAFTIAFTIGLAGNS 60

Qy 61 MVVAIVAYKKORTDQVYILNLAVADLLLTLPFWAVNAVHGVGLGIMCKITTSALYT 120

Db 61 TVVAIVAYKKRRTKTDVYILNLAVADLLLTLPFWAVNAVHGVGLGIMCKVTSALYT 120

Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWICFCVWMAAILLSIPQLVFTVND 180

Db 121 VNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWICFCVWMAAILLSIPQLVFTVNH 180

Qy 181 NARCIPIPPRYLGTSMKALIQMLEICIGRVDFLNGVCYFTARTLMKNPKIKSRPLK 240

Db 181 KARCVPFIFPHLGTSMKASIQILEICIGFIIPFLINAVCYFITAKTLIKMPNKKSQPLK 240

Qy 241 VLLTVVIVFTQLPVNIYKFCRADIIYSLITSCNMSKRMIDIAIOVTESIALFHSLCLNP 300

Db 241 VLFTVVIIVFTQLPVNIYKFCQADIIYSLITDCMSKRMIDVIAIQITESIALFHSLCLNP 300

```
Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVVEFPFDSEGPTEPTSTFSI 350
      :||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQSVVEFPFESEDATEPTSTFSI 350
```

RESULT 2

B55735
lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schwickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: B55735; M01D:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:131581; NTD:q468319; PIDN:AAA74231.1; PID:q468320
R:Burgstahler, R.; Kempkes, B.; Staebue, K.; Lipp, M.
Submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transa
A:Reference number: S52443

Query Match	36.2%;	Score 659;	DB 2;	Length 378;
Best Local Similarity	38.7%;	Pred. No. 4.5e-49;		

QY	1	MALEONQSTDYVYENENMGTQYDSQVELICKEDVREFAKVLFPVFLTVFVIGLAGNS	60
Db	21	VCLCODEVTDYIGDNT---TVDYTFESLCSKKVRNFKAMFLPIMYSIIICFVGLLNG	77
QY	61	MVAIYAYKKQRKTQVYILNLAVADLILLTLFPWAVNAVHVGLCKIMCKTISALYT	120
Db	78	LNVLYTYFFKRLKTMQTYILNLAVADILFLTLFPWASAKSVWFGVHCKLFIAYIK	137
QY	121	LNFGVSGMFLACISIDRYAVATKVPSS---QSGVGKPCWIIICFCVWMAAILLSIPOLVEY	176
Db	138	MSFSGMILLCLCISIDRYAIVQAVSAHRHRAVLLISKLSCVGIWIIATVLSIPELLYS	197
QY	177	TVNDNA-----RCPIPRYLGTSMKALIOMLCIGFVVPFLMGVCYFTARTLMKMP	231
Db	198	DLORSSSEQAMRCLSTEH---VEAFITTIQVAMVIGELVPLLAMSFYCVLIIRTLQAR	254
QY	232	NKITSRLPKVLLTWVIVFIVTQLPYNIIVFCRAIDIISLITSNMKSRMDIAQTVESTI	291
Db	255	NFERKAKVLIIVAVVVFIVFQLPYNGVGLVLAQTVANFNITSTCELSKQLNIAYDVYSL	314
QY	292	ALFHSCNLILYVFMGASFKNYVMKAKYKG-----SW-----RRORQSVEEFPFD	337
Db	315	ACVRCCVNPFLYAFIGVKFENDFLFKLKDGLCSOEQLQWSSCRHIRRSSMVE-----	369
QY	338	SEGTEPTSTFS	349
Db	370	-----AETTTFSS	377

RESULT
A55735
3

G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1995 #sequence_revision 07
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Goddard
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11,
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:q46034
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match	35.7%	Score 650;	DB 2;	Length 378;
Best Local Similarity	38.3%	Pred. NO. 2.7e-48;		
Matches 140;	Conservative	67;	Mismatches 125;	Indels 34;
				Gaps 8;

QY	5	QNQSTDYYYENENMGTYDYQSVELICIKEDVREFAKVFLPVFLTTIVFVIGLAGNSMWVA	64
Db	25	QDEVTDDYIGENT---TVDYTVESGCKFDKDNFNAWFLPLMYSVICFVGLLGNGLVIL	81
QY	65	IYAYKKORTKTDYVILNLAVADLLLTLPFWAVNAVHGWVLGKIMCKITSALYLTNFV	124
Db	82	TYFYRKLKMTDYLNLAVADILFLLLPFWAYSEAKSWIEGVLCRGIFGYIKLSFF	141
QY	125	SGMQFLACISIDRYAVTVKPSQSG-----VGKPCWIIICFCVMAAILLSIPQLVFVT	177
Db	142	SGMLLLCISIDRYAIVQAVSRHRHRAVLLISK---LSCVGMWALFLSLPELLYSG	198
QY	178	VDNA-----RCPIPRYLGTSKAL--IOMLEICIGFVVPFLMGVCYFITARTLMK	230
Db	199	LQNSGDETLRC-----SLVSAQVEALITIQVAQMVGFLVPLMASFVCLIIIRTLQA	253
QY	231	PNKISRPLKVLTVTVFVLTQLPYNIYKFCRAIDIIYSLITSCNWSKRMDAIOVTES	290
Db	254	RNFERKAIKVIIAVVVFVTFVQLPNGVVLVAQTAVANFNITNSSCETSQOLNAYDVTYS	313
QY	291	IALFLSCHLPILYVFMGAGFKNYVMKVAKYGSMRROR-----QSVEEFFPDSBGPTE	343
Db	314	LASVRCCVNPFLYAFYGVFRSDFLFLKFDLCLSQERLHWSRCHRVNASVSMB--AE	371
QY	344	PTSTFS	349
Db	372	TTTTFS	377

RESULT

A45680
G protein-coupled peptide receptor EBI-1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R.Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled receptor
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BI>
A:Cross-references: GB:L08176; NID:gl83484; PID:gl83485
A:Experimental source: B-Lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	35.3%;	Score 643;	DB 2;	Length 378;
Best Local Similarity	39.0%;	Pred. No. 1.1e-47;		

RESULT 7

RESULT 8
YES 100

probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C/Accession: J58186
R/Harrison, J. K.; Barber, C. M.; Lynch, K. R.
Neurosci. Lett. 169, 85-89, 1994
A/Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spleen
A/Reference number: J58186; MUID:94323113
A/Accession: J58186
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-354 <RES>

C; Superfamily: vertebrate rhodopsin
C; Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g4398603
C; Keywords: G protein-coupled receptor

c, keywords: a protein-coupled receptor

Query Match	28.8%	Score 524;	DB 2;	Length 354;
Best Local String	26.0%	Score 524; <td>DB 2; <td>Length 354;</td> </td>	DB 2; <td>Length 354;</td>	Length 354;

Best local similarity 36.9%; Pred. No. 1./e-37;
Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps

QY 22 YDYSQVELICIKEDVREFAKVFELPVELTIVEIGLAGNSMVVAIYAYVKKQRTDVIIL 81

Db 13 FEYDDSAEACYLGVAFGTIFLSIFYSLVTFGLVGNLLVVLALNSRKSSTIDYLL 72

QY 82 NLAVADLLLLFTLPFWAVNAVHGVLGKIMCKITSAITYLTNEVSGMQLACISIDRYAV 141

D_b 73 NLALSDLLFVATLPFWTHYLISHEGLHNACKLTTAFFIGFFGFFITVISIDRYLAI 132

Qy 142 TKVPS-----QSGVGKPCWICFCVWMAAILLSIPQLVFYTVNDNARCIPIFPRLGT 194

Db 133 VLAANMNNRTVQHG-----TISLGVAAAILVASQFMETKRRDN-ECLGDYPEVLQE 186

QY 195 SMKALIQMLEICIGFVVPFLINGVCYFITARTLMKMPNIKISRPLKVLTVVIVFIVTQL 254

Db 187 IWPLRNSVNILGFVLPLLIMSECFYFRVITLFSCNRKKARAIILLVVVFLEWT 246

QY 255 PYNIVKFCRAIDIYSLITSCNWSKRMEDIAIQVTESTALFHSLCPILYVFMCAFKNYV 314

Db 247 PYNIVIFLETLK-FYNFFPGMKRDLRWALSVTETVAFSHCCLNPFYIAFACEKFRYL 305

QY 315 MKVAKK 320
:
|

Db 306 RHYLYNK 311

RESULT 9

JC4304
orphan G protein-coupled receptor - human

N;Alternate names: V28 protein
C;Species: Homo sapiens (man)

C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304

R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 293-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

A:Reference number: JC4304; MUID:96011651
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:9665580; PIDN:AAA91783.1; PID:9665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
C:Genetics:
A:Gene: v28
A:Map position: 3pter-p21
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 522.5; DB 2; Length 355;
Best Local Similarity 36.4%; Pred. No. 2.3e-37;
Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

QY 22 YDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMWAIYAYKKQRTKTDVIL 81
DB 12 FEYDDLAEEAGYIGDIVVFGVIFSYFISVFAIGLVGNLLVAFALTNKKPKSVTDIYL 71
QY 82 NLAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLNFEVSGMQLACISIDRVAV 141
DB 72 NLASDLLFVATLPFWTHYLINKEGLHNAMCKETTAFFGFGSIFFIIVISIDRYLAI 131
QY 142 TKVPS-----QSGVGKPCWICFCVWMAAILLSIPQLVFTVNDNARCIPIPRYLGT 194
DB 132 VLAANSNNRTVQGV-----TISLGWMAAAILVAAPQFMFTOKEN-ECLDGYPEVLQE 185
QY 195 SMKALIQMLEICIGFVVFPFLMGVCVFTARTLKMKNISRLKVLKLVTVVIVFTQL 254
DB 186 IWPVLARVETNFGLFLLPLLIISYCFRIQTFLSCNKHKKAKAILLVIVVFFLWT 245
QY 255 PYNIVAFCAIDIIYSILTSNCKSKRMIDIAIQVTESTIALFHSCLNPLIYVFMGASFKNYV 314
DB 246 PYNVMIFLETLK-LYDFFPSCDKRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRYL 304
QY 315 MKVAKKYG 322
DB 305 YHL---YG 309

RESULT 10
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
A:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus

F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

Query Match 28.7%; Score 522.5; DB 2; Length 360;
Best Local Similarity 33.7%; Pred. No. 2.3e-37;
Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;

QY 3 LEQNQSTDYEEENMGNTDYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMV 62
DB 1 MNATEVDTTQDETIVNSYYPFESMPKPCFKAFGEVFLPPLYSLVFLGLFGNSV 60
QY 63 VAIYAYKKQRTKTDVILNAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLN 122
DB 61 VLVLFKYKRUKSMTDVLNLAISDLLFVLSLFWGYAAQDWVFGGLCKIVSNMVLVG 120
QY 123 FVSGMQFLACISIDRYVAVTKV-----PSQSGVGKPCWICFCVWMAAILLSIPQLVF 175
DB 121 FYSGIFFIMLSIDRYLAIVHAVFSLKARTLTGV-----ITSLLTWSVAVFASLPGLLF 175
QY 176 ---YTVNDNARCIPIPRYLGTSMKALIQMLEI-CIGFVVPFLMGVCVFTARTLKM 231
DB 176 STCTENHNTYCKTOYS--VNSTTWKVLSSLEINVLGLIPLGIMLFWYSMIITLQHC 233
QY 232 NIKISRLPKVLLTVVIVFIVTQLPYNIKFCRAIDIIYSILTSNCKSKRMIDIAIQVTE 291
DB 234 NEKNRAVRMIFGVVFLGFWTPYNNVLFLET-LEVEVLQDCTLERYLDYAIQATETL 292
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKV 317
DB 293 GFICHCLNPLIYFELGKFKRYITQL 318

RESULT 11

B55733
G protein-coupled receptor GPR2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C:Accession: B55733
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Helber, M.; Cheng, R.; Heng, H.H.Q.; Tsui
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:95154831
A:Accession: B55733
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <MAR>
A:Cross-references: GB:U13667
C:Genetics:
A:Gene: GDB:GPR2
A:Cross-references: GDB:371708; OMIM:600240
A:Map position: 17q21.1-17q21.3
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 28.5%; Score 518.5; DB 2; Length 354;
Best Local Similarity 33.9%; Pred. No. 5e-37;
Matches 121; Conservative 65; Mismatches 142; Indels 29; Gaps 7;

QY 12 YEEENMGNTDYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMWAIY-AYYK 70
DB 5 HYSGDE-EDAYSAPLPCLCYKADVQAFSRAFPQSVSLTVAALGLAGNLVLATHLAAR 63
QY 71 QKRTKTDVILNAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLNFEVSGMQFL 130
DB 64 AARSPTSAHLQLALADLLALTLPFAAAGALQGSLSATCRTISGLYSASFAGFLFL 123
QY 131 ACISIDRYVAVTKV-----PSQSGVGKPCWICFCVWMAAILLSIPQLVFTVND---NAR 183
DB 124 ACISADRYVAIARALPAGPRPSTPGR-AHLVSVIWMLLSLLALPALLFSQDQREGORR 182

QY	184	CTIPRPYLGTSKALIQLEICIGFVVPFLIMGVCYFIARTLMKNPNIKISRLPKVLL	243
Db	183	CRLEIEGTLQTVKGASAVAQFALPLGVWVACVALLGRITLLAARGPERRALRVVV	242
QY	244	TVVIVFIVTQLPYNIKFCRAIDIIYSLTSCNNKRMKDIAIOVTSIALFHSLNPILY	303
Db	243	ALVAAVFVQLQPLYSIALLLDTPADLLAARERSCPAKRKDVALLVTSGLALARGLNPVLY	302
QY	304	VPMGASFKNNYMKVAK-----XYGSMRQRQSQVEEFPDSCGPTPTSTFSI	350
Db	303	AFGLGPFQDRLRLRGSSPGPQRGCPRRPLUS-----SCSAPTETHSL	350

RESULT 12

A53752

Interleukin-8 receptor (Clone 58La) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: A53752

R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava, J. *Biol. Chem.* 269, 12391-12394, 1994

A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A:Reference number: A53752; MUID:94230294

A:Accession: A53752

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-358 <PRA>

A:Cross-references: GB:124445; NID:9437661; PIDN:AAA31378.1; PID:9437662

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	28.1%	Score 511;	DB 2;	Length 358;
Best Local Similarity	32.3%;	Pred. No. 2.2e-36;		
Matches 116;	Conservative 72;	Mismatches 139;	Indels 32;	Gaps 8;

Qy	10	DYYTEENMGTYDYSOYELI-----CIREVREFAKVPFLPTIVFVEIGA 57 : : : :
Db	8	NYSYE--DFG--DFSNSYSTDLPTLLDSAPCRSELETNSYVVLIYVI-LVFLSUL 62 : : : :
Qy	58	GNSMVAIAIYKKQRTKTDOYIILNLAADLLLFTLPFWAVNAHVGLWKIMCKITSA 117 : : : : : : : : :
Db	63	GNSLMLVLILYSRSTCVTDVYLLNLAIADLLPATPLPIWAASKVHGWTGTPCLCKVSL 122 : : : : : : : : : :
Qy	118	LYTLNFVSGMOQLACISIDRYAV----TKPVSQSVCVKPCWICFCVMAAILLSIPQ 172 : : : : : : : :
Db	123	VKEVNFVSGILLACISVDRIYAIVHATMTIQRLVK----FICLSMWGSYLILSPI 178 : : : : : : : : : :
Qy	173	LVFYTVNDNARCIPFPVILGTS---MKALIOMLEICIGVVPFLIMGVCYFITARTLMK 229 : : : : : : : : : :
Db	179	LFRNAIFPPNSSPVCYEDGNSTAKRWVIRLPOTFGFIPLLVMLCYVFTURTFUQ 238 : : : : : : : : : :
Qy	230	MPIKISRPLKULLTVVIVTQLPYNIVKFCRAIDIYLSITSNMSKRMDIAQVTE 289 : : : : : : : : :
Db	239	AHMGOHRAMRVIFAIVLFILCWLPYNELVLLTDTLMRTHVJQCERENDIDRALDATE 298 : : : : : : : : :
Qy	290	SIALFHSCLNPIILYPWGASFRNYMKVAKKYGSWRRQ---QRSVEEFPFDSEGPEPT 345 : : : : : : : : :
Db	299	ILGFHSCLNPIIAYFIGQVGRGLLKILAAHLGISKEFLAKESRPFSVASSSGNTSIT 357 : : : : : : : : :

RESULT 13
JQ1231
interleukin-8 receptor - rabbit
C-species: Oryctolagus cuniculus (domestic rabbit)
C-date: 31-Mar-1992 #sequence_revision 31-Mar-1992
C-accession: JQ1231; A46483
R-Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lym
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A-title: Molecular characterization of the interleukin-8 receptor.
A-reference number: JQ1231; MUID:91378994
A-accession: JQ1231

A: Molecule type: DNA
A: Residues: 1-355 <BEC>
A: Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
J: Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J: Immunol. 148, 1261-1264, 1992
A: Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
A: Reference number: A46483; MUID:92148149
A: Accession: A46483
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-355 <LEE>
A: Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A: Experimental source: neutrophils
A: Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:P:81530)
C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor; transmembrane protein

Query Match	27.6%	Score	501.5;	DB	2;	Length	355;
Best Local Similarity	33.1%	Pred. No.	1.4e-35;				
Matches	107;	Conservative	70;	Mismatches	127;	Indels	19;
						Gaps	6;

Query Match	27.6%	Score 501.5	DB 2	Length 355
Best Local Similarity	33.1%	Pred. No. 1.4e-35		
Matches 107	Conservative 70	Mismatches 127	Indels 19	Gaps

Qy	12	YYEENEMNGT-----YDY	SOYELICIKEDVRFEAKVFLPV	FTIVPVIGLAGNSMVVAI	65	
Db	14	WFEDEFANATGMPPEVKDYS--	PCLVVVTQTLNKVVV----	VIVALFLLSLLGNSLVMLV	68	
Qy	66	YAYYKKORTQDVILNLAVADLL	LLTFLPFMAVNVGHVGLCKM	CKITTSALYTLNFVS	125	
Db	69	ILYSRSNRSTVDYLLNLAMAD	LLFALTMFINAVSKEGWI	FGTCLCKVVSVLKVEFNYS	138	
Qy	126	GMQFLACISIDRIVAV---TK	VPSQSGVGKPCWICFVMM	AAIILSIPOLVFYTVNDNA	182	
Db	129	GILLACISVDRLVAIVHATRT	LTKQ--RHLVVFICILG	IWALSLLSFLFLRQVFS	186	
Qy	183	RCIPIFPRYLG---TSMKAL	IOLEICIGVVPFLTMGV	CYFTTARTLKMPNKISRPL	239	
Db	187	NSSPCVCEYDLGHNTAKRM	VMVLRILPHTFCGFLPL	LVNLFCYFTLTLFQA	HMGQKHRA	246
Qy	240	KVLLTVVIVFIVTQDPYNI	VKFCRAIDIYSLITS	CNMSKRMDIATQVTEST	IALFHSCLN	299
Db	247	RVFAVVLFLCGLPYNLL	ADTLMRTHVTOETCOR	RNDIDRALDATEILG	FLHSCLN	306
Qy	300	PILYFVWGASFKNVMVKAK	YK 322			
Db	307	PIIYAFIGNFRNGFLKML	AAARG 329			

RESULT 14

A45747 neuropeptide Y/peptide YY receptor Y3 - human
 Nt:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
 R:Referspieler, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L
 Genomics 16, 707-712, 1993
 A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a
 A:Reference number: A45747; MUID:93315164
 A:Accession: A45747
 A:Molecule type: mRNA
 A:Residues: 1-352 <FED>
 A:Cross-references: GB: T929293; NID:g292516; PIDN:AAA16617.1; PID:g292517
 R:R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
 J. Biol. Chem. 269, 232-237, 1994
 A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl
 A:Reference number: A53103; MUID:94103215
 A:Accession: A53103
 A:Molecule type: mRNA
 A:Residues: 1-352 <LOE>
 A:Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
 R:R:Herzog, H.; Hört, Y.J.; Shine, J.; Selbie, L.A.
 DNA Cell Biol. 12, 465-471, 1993
 A:Title: Molecular cloning, characterization, and localization of the human homolog t
